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Sequence Listing

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Botstein, David
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Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.

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Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
tgagcttctg gtgcntttg gctctaattc tggccacaca gagaancagt 100
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
ggcccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350
tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450
gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgacggaatc ccgggctggg tctcctgggt tngacaagat aaacccccag 50
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100
agttcacctt ngtttgnatg gntctgtcaa ctacgctnt gtttcgtgat 150
gttttgagaca ccaaagtgt ttgagaaaat tttgatagac atnatcgag 200
tggantttgc ctttgacagaa ntttgnngtg ttcctttgcg gattttctcc 250
tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50
acactgaaga aaaccttngt ccttgccccc agntttgtgn tgcggatnat 100
cgctctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150
agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattcttcc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttcgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
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gcctgcctgg gagcctgtc cctgctcagc tgcgcgtcct gcctctgcgg 100
ctctgcccc tgcatcctgt gcagctgtg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300
tcgactgtgg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc 350
gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgctg 400
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450
ttaagttcct gatcctggtg ggctcaccg tgggtgcctt ctacatccct 500
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cctcttcctc ctcatccagc tgggtgctgct catcgacttt gcgcactcct 600
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650
tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgctgatcgc 700
ggcgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750
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atcgtgctg tctgcccac ggtccaggac gccagccca actcgggtct 850
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950
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gcagggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
tcacctacag ctactccttc ttccacttct gcctggtgct ggctcactg 1250
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gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
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tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500
caccaatcag ccaggctgag cccccacccc tgccccagct ccaggacctg 1550
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caggctcctg cagagcccca tcccccgcc acaccacac ggtggagctg 1650
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 agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc 1750
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc ccccagggga ccctgcccc ttcttggaact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900

a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser	1	5	10	15
Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro	20	25	30	
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe	35	40	45	
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly	50	55	60	
Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75	
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90	
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105	
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120	
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135	
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150	
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165	
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180	

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu	185	190	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr	200	205	210
Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe	215	220	225
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala	245	250	255
Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser	455		

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gccgcctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcatccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
cttcttccac ttctgcctgg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcacc acgg 24

<210> 25
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tgcagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctcgtacagt tacgctctcc 100
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150
aggctcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250
actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattaccggg aatctggatg ggaccgcctc cgggagctgt 350
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550
cgaggcttca ttcgttatgg ctggcgctgg ggttgagaaa ctgcagtgtt 600
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700
tttaggataa acgtaggcct gcgtggcctg gtggctgggtg gcataattgg 750
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acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
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 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
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 gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100
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 gtactctcac tttacttata cttaaattta aatacatact tatgtttgta 1250
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 t 1351

<210> 28

<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

Met	Glu	Val	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Phe	Leu	Cys	Arg	Ala	1	5	10	15
Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala	20	25	30	
Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45	
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60	
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75	
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90	
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105	
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120	
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135	

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn
				140					145					150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu
				155					160					165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg
				170					175					180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly
				185					190					195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln
				200					205					210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg
				215					220					225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu
				230					235					240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg
				245					250					255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu
				260					265					270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp
				275					280					285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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ctattaccgc gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100

tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200

catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250

ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300

ttcgttcacg gctggcgccg aacc 324

<210> 30

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
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accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
gcggtctccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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ccaccacagt ctgcgttgct gcccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300
tccgagtggc cggcgtggc attgcagtgg gcattcttctt gttcctgatt 350
gcttttagtg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400
tttttatatg attattctgt tacttgattt tattgttcag ttttctgtat 450
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500
gttggttgga acaatacggc aagtgcctga aatgacatcc agagaaatct 550
aaactgctgt gggttccgaa gtgttaacct aaatgacacc tgtctggcta 600
gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650
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cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
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taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900
ttattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950
ttttctttcc gttgctgaaa aatatttgaa acttggtgct tctgaagctc 1000
ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050
cctttcttag catttttacc tgcagaaaaa ctttgatagg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcaactgggtat aattatatgt 1150
 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200
 taaaatcaga aagtatgaga tcctgttatg ttaagggaaa tccaaattcc 1250
 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
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 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450
 acattttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500
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 aagactgcat ttttaaacia gttagtatta atgcgttggc ccacgtagca 1600
 aaaagatatt tgattatctt aaaaattgtt aaataaccgtt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala
 1 5 10 15
 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30
 Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val
 35 40 45
 Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala
 50 55 60
 Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu
 65 70 75
 Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe
 80 85 90
 Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly
 95 100 105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	110	115	120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	125	130	135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	140	145	150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	155	160	165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	170	175	180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	185	190	195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							200		

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
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 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100
 tagccttgaa ccaggagcaa cagggtcagn ttntggaggt tgggttgaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300
 gaggttttga gatttgttgg tggcattggc ctgttnttca gttttacaga 350
 gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 27

<223> unknown base

<400> 38

aatcccaaat tccccaattt ttttgnctt tttagggaaa gatgtgttgt 50
ggtaaaaagt gttagtataa aaatgataat ttactttag tcttttatga 100
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgag 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagtcttc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

atgattattc tgttacttgt atttattggt cagttttatg gtatcttgag 50
cttgttttagc ccctgaaacc aggagcaaca gggnnacagc tcctggaggt 100
tggttggtgcaa caatcacggc caagtgactc cgcaaagac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200
tggtctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40
accacgtct gcgttgctgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
aggaaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ggccccaaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
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gacgctgcag tgtgaggac ctgtctgcac tgaggagagc agtgccaca 150
cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacaggggaat tctccatcac 400
cgtggtacaa aaggcagaca gcgggcacta ccaactgcagt ggcattcttc 450
agagccctgg tcctgggatc ccagaaacag catctgttgt ggctatcaca 500
gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550
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tgcagagggtc agctgcccgc ctctcttct cttctacaa ggatggaagg 650
atagtcaaaa gcagggggct ctctcagaa ttccagatcc ccacagcttc 700
agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750
aagtttgaa acagagcccc cagctagaga tcagagtga ggggtgcttc 800
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cctcatctgt atcaccagat gggccttctt ctcaaacaca tgcaggatgt 1000
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agaattagag ttagctata attgtgtatt ctctcttaac acaacagaat 1300
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ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850
 cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccct 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
 ttgtagccta a 2061

<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 45
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
 20 25 30
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
 80 85 90
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
 110 115 120
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val
 155 160 165
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala
 170 175 180
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 46
 tgggctgtgt cctcatgg 18

<210> 47
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 47
 tttccagcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagt gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcccacgcg tccgcccacg ggtccgcca cgcgtccggg 50
ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
gtgtaacagg accttgga aa ggggatgtga atcttcctg cacctatgac 250
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350
agcaggcaaa gtaccagggc cgctgcatg tgagccacaa ggttccagga 400
gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450
cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500

ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550
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caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550
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ctttgccctg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850
ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactctc 1900

tctaaatacc agaggggaaga tgcccatagc actaggactt ggtcatcatg 1950
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100
 agggttcagt tctgctcctc cactataagt ctaatgttct gactctctcc 2150
 tgggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr
 185 190 195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	200	205	210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	215	220	225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	230	235	240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	245	250	255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	260	265	270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	275	280	285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	290	295	300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	305	310	315
Val	Tyr	Glu	Ala	Ala	Arg										320		

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 tatccctcca attgagcacc ctgg 24

<210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 gtcggaagac atcccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 55
cttcacaatg tcgctgtgct gctc 24

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
agccaaatcc agcagctggc ttac 24

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58
<211> 2458
<212> DNA
<213> Homo sapiens

<400> 58
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cgccccggcac atggctgcag ccacctcgcg cgcaccccga ggcggcgcg 100
ccagctcgcc cgagggtccgt cggagggcgcc cggccgcccc ggagccaagc 150
agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200
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ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450
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gattcatctg taaaaaggca tcttattgtg ctttagacc agagtaaggg 1550
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ctaactcac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000
aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050
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cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150
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 agaaaaaggg atctaggaat gctgaaagat taccacaacat accattatag 2250
 tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300
 tagaaagggg gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350
 cgggcatggg gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400
 gtgagccgag attatgccat tgcaactccag cctgggtgac agagcgggac 2450
 tccgtctc 2458

<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

Met	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Val	Ser	Tyr	Tyr	Val	Gly	1	5	10	15	
Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys	20	25	30	
Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp	35	40	45	
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln	50	55	60	
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu	65	70	75	
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu	80	85	90	
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp	95	100	105	
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val	110	115	120	
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro	125	130	135	
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr	140	145	150	
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr	155	160	165	
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro				

170	175	180
Pro Lys Ser Arg Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu	
185	190	195
Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala	
200	205	210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val	
215	220	225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly	
230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	
245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro	
260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	
275	280	285
Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly	
290	295	300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln	
305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	
320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro	
335	340	345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro	
350	355	360
Ser Met Ile Pro Ser Gln Ser Arg Ala	Phe Gln Thr Val	
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

ccagtgcaca gcaggcaacg aagc 24

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
actaggctgt atgcctgggt gggc 24

<210> 62
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 62
gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63
<211> 3534
<212> DNA
<213> Homo sapiens

<400> 63
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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

Met	Gly	Thr	Ser	Pro	Ser	Ser	Ser	Thr	Ala	Leu	Ala	Ser	Cys	Ser	1	5	10	15
Arg	Ile	Ala	Arg	Arg	Ala	Thr	Ala	Thr	Met	Ile	Ala	Gly	Ser	Leu	20	25	30	
Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val	
				575					580					585	
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe	
				590					595					600	
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile	
				605					610					615	
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu	
				620					625					630	
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp	
				635					640					645	
Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu						
				650					655						

<210> 65
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
 gtagcagtgc acatggggtg ttgg 24

<210> 66
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 66
 accgcacatc ctcagtctct gtcc 24

<210> 67
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 67
 acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68
 <211> 2412
 <212> DNA
 <213> Homo sapiens

<400> 68

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ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgatttgaaa 200
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atgtgtgct tgacgtatta ttgtccttg attccaaata atatgtttcc 2350
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catccactga aa 2412

<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

Met	Gly	Glu	Asn	Asp	Pro	Pro	Ala	Val	Glu	Ala	Pro	Phe	Ser	Phe
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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35				40						45

Leu	Lys	Phe	Phe	Pro	Ile	Ile	Val	Ile	Gly	Ile	Ile	Ala	Leu	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly		
65	70	75
Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala		
80	85	90
Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr		
95	100	105
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe		
110	115	120
Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly		
125	130	135
His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr		
140	145	150
Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe		
155	160	165
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys		
170	175	180
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala		
185	190	195
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg		
200	205	210
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu		
215	220	225
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His		
230	235	240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala		
245	250	255
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile		
260	265	270
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His		
275	280	285
Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg		
290	295	300
Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr		
305	310	315
Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu		
320	325	330
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala		

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Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala	Ala
	350	355	360
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp Val	Tyr
	365	370	375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu	Thr
	380	385	390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu	Val
	395	400	405
Cys Gln Glu Arg	Arg Leu Trp Lys Leu	Val Gly Ala Thr Ser	Phe
	410	415	420
Gly Ile Gly Cys	Ala Glu Val Asn Lys	Pro Gly Val Tyr Thr	Arg
	425	430	435
Val Thr Ser Phe	Leu Asp Trp Ile His	Glu Gln Met Glu Arg	Asp
	440	445	450

Leu Lys Thr

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cggtcaatgc agaaatgata cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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gctcagcggc ggcgcgggcg ctgcgcgagg gctccggagc tgactcgccg 200
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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	35	40	45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	50	55	60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	65	70	75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	80	85	90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	95	100	105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly	110	115	120	

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctaccaggga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150

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aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaaggggtt gggcccagtg tcccctttcc ccagtgtacac ctcagccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

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gagaccctgc caccattcc atntccatcc aag 483

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<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 76

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<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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catgagcatg tgcacggc 18

<210> 78
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<400> 78
tacctgcacg atgggcac 18

<210> 79
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<220>
<223> Synthetic oligonucleotide probe

<400> 79
cactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 81
tccctgttgg actctgcagc ttcc 24

<210> 82
<211> 19
<212> DNA
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<220>
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<400> 82
cttcgctggg aagagtttg 19

<210> 83
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<210> 84
<211> 1714
<212> DNA
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<210> 85
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 85
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 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
 35 40 45
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
 50 55 60
 Ala Leu Leu His Leu Tyr His
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<210> 86
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
acgggcacac tggatcccaa atg 23

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggtagagatg tagaaggga agcaagacc 29

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89
<211> 2956
<212> DNA
<213> Homo sapiens

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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

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Ala	Ala	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Leu	Gly	His	Gly	Gly
				20				25					30

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
				35				40						45

Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro	50	55	60
His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile	65	70	75
Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly	80	85	90
His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys	95	100	105
Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp	110	115	120
Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly	125	130	135
Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys	140	145	150
Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu	155	160	165
Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu	170	175	180
Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser	185	190	195
Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile	200	205	210
Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro	215	220	225
Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val	230	235	240
Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser	245	250	255
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Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser	275	280	285
Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly	290	295	300
Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala	305	310	315
Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn	320	325	330

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp
350 355 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu
410 415 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
425 430

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91

atgttcttcg cgccctggtg 20

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

ccaagccaac acactctaca g 21

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aagtggtcgc cttgtgcaac gtgc 24

<210> 94

<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtcaaaggg gatatatcgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

<400> 96
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aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150
atttcaccag gacccaaagg agatgatggg gaaaaaggag atccaggaga 200
agagggaaaag catggcaaag tgggacgcat gggggccgaaa ggaattaaag 250
gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300
attgggaaga aggggtgaca aggggaaaaa ggtttgcttg gaatacctgg 350
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ctcatcgtg actatgttgc caagagtggc ttctttcggg tgttcattgg 650
cgtgaatgac cttgaaaggg agggacagta catgtccaca gacaacactc 700
cactgcagaa ctatagcaac tggaatgagg gggaaccag cgaccctat 750
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agagtgccat cttaccatgt actttgtctg tgagttcatc aagaagaaaa 850
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 cagttattgt tatccatcct ttttttcctg attgtactac atttgatctg 950
 agtcaacata gctagaaaaat gctaaactga ggtatggagc ctccatcatc 1000
 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
 Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu
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 Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn			
	215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser			
	230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly			
	245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys			
	260	265	270
Glu Phe Ile Lys Lys Lys Lys			
	275		

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
 cgctgactat gttgccaaga gtgg 24

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 99
 gatgatggag gctccatacc tcag 24

<210> 100
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 100
 gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101
 <211> 2574
 <212> DNA
 <213> Homo sapiens

<400> 101
 gggttctatcg attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctcgacctcg acccacgcgt ccgctgctct ccgcccgtgt ggagtgggtg 100
gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150
gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200
agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250
gctccatggc tgccctcctg ctgctgcccc tgctgctgtt gctaccgctg 300
ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350
cttggccttt gcggtgcgag ctctgtgctg caaaagggct cttcgagctc 400
gcgccctggc cgcggctgcc gccgaccgg aaggtcccga ggggggctgc 450
agcctggcct ggcgctcgc ggaactggcc cagcagcgcg ccgcgcacac 500
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ggcagcgccg ggagccggag atgcagcggc cggaagcggc gcggagtttg 700
ccggagggga cggtgccgcc agaggtggag gagccgcgc ccctctgtca 750
cctggagcaa ctgtggcgct gctcctcccc gctggcccag agtttctgtg 800
gctctgggtc gggctggcca aggccggcct gcgcactgcc tttgtgcca 850
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tgtcaaccag ccccgagca aggcagaacg tggccataag gtccggctgg 1450

cagtgggcag cgggctgcgc ccagatacct gggagcgctt tgtgcggcgc 1500
 ttcgggcccc tgcaggtgct ggagacatat ggactgacag agggcaacgt 1550
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 cgatgaccaa ggttttctcc gcttccatga tcgtactgga gacaccttca 1900
 ggtggaaggg ggagaatgtg gccacaaccg aggtggcaga ggtcttcgag 1950
 gccctagatt ttcttcagga ggtgaacgtc tatggagtca ctgtgccagg 2000
 gcatgaaggc agggctggaa tggcagccct agttctgct cccccccacg 2050
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 tatgcccggc cccgattcct caggctccag gagtctttgg ccaccacaga 2150
 gaccttcaaa cagcagaaag ttcggatggc aaatgagggc ttcgaccca 2200
 gcacctgtc tgacctactg tacgttctgg accaggctgt aggtgcctac 2250
 ctgcccctca caactgcccg gtacagcgcc ctctggcag gaaaccttcg 2300
 aatctgagaa cttccacacc tgaggcacct gagagaggaa ctctgtgggg 2350
 tgggggccgt tgcaggtgta ctgggctgtc agggatcttt tctataccag 2400
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 ctctgacct aaaaaaaaaa aaaaaaaaaa aaaaaaaaag ggcggccgcg 2500
 actctagagt cgacctgcag tagggataac agggtaataa gcttggccgc 2550
 catggcccaa cttgtttatt gcag 2574

<210> 102
 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser
 1 5 10 15
 Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
 20 25 30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380		385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp
500		505	510
Val Thr Thr Gly	Glu Pro Ile Arg Asp	Pro Gln Gly His Cys	Met
515		520	525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu	Leu Val Ala Pro Val	Ser
530		535	540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu	Ala
545		550	555
Gln Gly Lys Leu	Leu Lys Asp Val Phe	Arg Pro Gly Asp Val	Phe
560		565	570
Phe Asn Thr Gly	Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe	Leu
575		580	585
Arg Phe His Asp	Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly	Glu
590		595	600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp	605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His	620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His	635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu	650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu	665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn	680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu	695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr	710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile	725	730	

<210> 103
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 103
 gagagccatg gggctccacc tg 22

<210> 104
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 104
 ggagaatgtg gccacaac 18

<210> 105
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
cctgtgttaa gctgaggttt cccctagatc tcgtatatcc ccaacacata 50
cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
acgcgcgcac acacactcgc tctcgtttgt ccattctcct cccgggggag 150
ccggcgcgcg ctccacactt tgccgcacac tccggcgagc cgagcccgc 200
gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250
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gcccttggtg gcttgccatc gtccatctgg cttataaaag tttgctgagc 400
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accacttttg tgtccaggca taagaaattt gacgaatttt tccgagagct 900
cctggagaat gcagaaaagt cactaaatga tatgtttgta cggacctatg 950
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caagcttgga ccggtgggtc acagacataa aagagaaatt gaagctctct 1750
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atggcaatga tgtcaatttc caggacacaa gtgatgaatc cagtggctca 2050

gggagtggca gtgggtgcat ggatgacgtg tgtccacgg agtttgagtt 2100
 tgtcaccaca gaggcccccg cagtggatcc cgaccggaga gaggtggact 2150
 cttctgcagc ccagcgtggc cactccctgc tctcctggtc tctcacctgc 2200
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 cactcttggc caatggacca tgccacaaaa acttacggtt ttctatgaga 2350
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 gggtgccaga ctgaactgct tctcttttcc ttcagctatc tgtggggacc 2450
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
 ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacggt 2550
 gtgagggttt tttttttctc atttaaaat 2579

<210> 109
 <211> 555
 <212> PRT
 <213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu	1	5	10	15
Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys	20	25	30	
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala	35	40	45	
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys	50	55	60	
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu	65	70	75	
Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90	
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105	
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120	
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135	
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150	

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp
440 445 450

Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met
455 460 465

Ala Leu Arg Val Met Thr Asn Lys Leu Lys Asn Ala Tyr Asn Gly
470 475 480

Asn Asp Val Asn Phe Gln Asp Thr Ser Asp Glu Ser Ser Gly Ser
485 490 495

Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe
500 505 510

Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg
515 520 525

Glu Val Asp Ser Ser Ala Ala Gln Arg Gly His Ser Leu Leu Ser
530 535 540

Trp Ser Leu Thr Cys Ile Val Leu Ala Leu Gln Arg Leu Cys Arg
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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

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<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113
<211> 4649
<212> DNA
<213> Homo sapiens

<400> 113
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cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150
tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200
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<210> 114
 <211> 515
 <212> PRT
 <213> Homo sapiens

<400> 114
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 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser
 35 40 45
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala
 50 55 60
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
 65 70 75
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
 80 85 90
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
 95 100 105
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro
 110 115 120
 Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln
 125 130 135
 Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro
 140 145 150

Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys	155	160	165
Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln	425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu	
				440					445					450	
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr	
				455					460					465	
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly	
				470					475					480	
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe	
				485					490					495	
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr	
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Gly	Ile	Gln	Glu	Ser											
				515											

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 115
 cccaacccaa ctgtttacct ctgg 24

<210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctctgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
 gccaccctac ctcagaaact gaaggagggt ggntattcaa cgcatatggt 50

cgg 53

<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086
<223> unknown base

<400> 118
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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly		20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr		35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr		140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser		170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
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Gly Lys Lys Gly Asn Glu Glu Lys
 335

<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

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ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtggaattg gtgaggagct ggcttaccag 200

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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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				20					25				30	

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40				45	

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55				60	

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<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

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<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaattg 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131
gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50
ggcagggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100
caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200
tccctggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250
cgtgctctat gattttctgca ttgtttgtat caccacctat gctatcaacg 300
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ccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500
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gcagacacct ggttcctcac tgctgccac tgctttgaaa aggagcagc 600
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gactcagccc tggggccgaa gaggtggggg tggctgccct gcagttgccc 700
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 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

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				20					25					30

Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn	50	55	60
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln	65	70	75
Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val	80	85	90
Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu	95	100	105
Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu	110	115	120
Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro	125	130	135
Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu	140	145	150
Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln	155	160	165
Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly	170	175	180
Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu	185	190	195
Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn	200	205	210
Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met	215	220	225
Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly	230	235	240
Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp	245	250	255
Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu	260	265	270
Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp	275	280	285
Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro	290	295	300
Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly	305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
									325						330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
									340						345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
									355						360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	
									370						375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	
									385						390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu	
									400						405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	
									415						420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	
									430						435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	
									445						450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	
									460						465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	
									475						480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu	
									490						495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu	
									505						510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg	
									520						525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser	
									535						540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu	
									550						555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser	
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Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gtttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggcgcgcc ccggccccca ttcggggccgg gcctcgctgc ggcggcgact 50
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ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150
gatgctgcgt cggcggggca gccctggcat ggggtgtgcat gtgggtgcag 200
ccctgggagc actgtggttc tgctcacag gagccctgga ggtccaggtc 250
cctgaagacc cagtgggtggc actggtgggc accgatgcca ccctgtgctg 300
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ggcagctgac agatacaaaa cagctggtgc acagctttgc tgagggccag 400
gaccagggca ggcctatgc caaccgcacg gccctcttcc cggacctgct 450
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agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600
gccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650
gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcaggg 700
gtgcccctga ctggcaacgt gaccacgtcg cagatggcca acgagcaggg 750
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acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950

attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137
<211> 316
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> 233
<223> unknown amino acid

<400> 137

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				20					25					30	
Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	
				35					40					45	
Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	
				50					55					60	
Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	
				65					70					75	
Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	
				80					85					90	
Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	
				95					100					105	
Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	
				110					115					120	
Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	
				125					130					135	
Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	
				140					145					150	
Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	
				155					160					165	
Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	
				170					175					180	
Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	
				185					190					195	
Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	
				200					205					210	
Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	
				215					220					225	

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln	
				230					235					240	
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	
				245					250					255	
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	
				260					265					270	
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala	
				275					280					285	
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln	
				290					295					300	
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile	
				305					310					315	

Ala

<210> 138
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 138
 ctggcacagc tcaacctcat ctgg 24

<210> 139
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 139
 gctgtctgtc tgtctcattg 20

<210> 140
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 140
 ggacacagta tactgaccac 20

<210> 141
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
tgcgaaccag gcagctgtaa gtgc 24

<210> 142
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
ttcgtgaccc ttgagaaaag agttggtggt aaatgtgcca cgtcttctaa 50
gaagggggag tcctgaactt gtctgaagcc cttgtccgta agccttgaac 100
tacgtttctta aatctatgaa gtcgaggagac ctttcgctgc tttttagagg 150
acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcgggc 200
ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250
agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300
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gtttaccctg ggcacccctg aggcctctcaa aggttgggac cagggcttga 450
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cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650
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aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800
gagttataga gatacatcta cccttttaac atagcactca tctttcaaga 850
gagggcagtc atctttaaag aacattttat tttatacaa tgttctttct 900
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 agtatattat actacaataa cattgtatca taagataaag tagtaaacca 1950
 gtctacattt tcccatttct gtctcatcaa aaactgaagt tagctgggtg 2000
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 tagtcccagc tactcgggag gctgagacag gagatttgct tgaacccggg 2200
 aggcggaggt tgcaagtgc caagattgtg ccactgcact ccagcctggg 2250
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<210> 145
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 145
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 20 25 30
 Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
 35 40 45
 Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
 50 55 60
 Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
 65 70 75
 Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
 80 85 90
 Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
 95 100 105
 Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
 110 115 120
 Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
 125 130 135
 Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
 140 145 150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
				200					205					210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

ctttccttgcc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gcccagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

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<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

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<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
				20					25					30
Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45
Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu

110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile	Met Asn Pro Pro Asp Arg	
125	130	135
His Arg Gly His Gly Lys Ile His Leu	Gln Val Leu Met Glu Glu	
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala	Val Ile Val Gly Ala Ser	
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile	Leu Val Leu Met Val Val	
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln	Lys Leu Ser Thr Asp Asp	
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Leu Lys Thr Glu Glu Glu Gly Lys Thr	Asp Gly Glu Gly Asn Pro	
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 ccnactaaca tctcagtcctc tgaaaatgca cagagatgcc tggctacctc 150
 gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcc 200
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 aatggctctg acgcccgcct gccctgcct tcaactcctg ctacacagt 300
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
 ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400
 tggagcgggt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
tcacggggct catctctttt tctcttttgt gccaccagg acggagcatg 50
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ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300
tcggtgatgc tgagaaacgt gcagccggag gatgagggga ttacaactg 350
ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgctgacct gcacctcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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cgcggaacca ggcgtcccg cggacgtca cccccagtg gtgctgggtcc 150
ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200
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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu		
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr		
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln		
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu		
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys		
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu		
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp		
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln		
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser		
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu		
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacggggc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
tcttcgcctt gatcgtgttc tcttgcattc atggtgaggg ctacagcaat 200
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<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162
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 Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly
 35 40 45
 Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val
 50 55 60
 Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly
 65 70 75
 Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala
 80 85 90
 Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val
 95 100 105
 Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe
 110 115 120
 Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro
 125 130 135
 Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr
 140 145 150

Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu
				155					160					165
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn
				170					175					180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr
				185					190					195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln
				200					205					210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr	
				215					220					

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

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<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaaggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
ccacgagtct aagcagatgt actgctgtt caaccgcaac gaggatgcct 50

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
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atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

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Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu				

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Thr Ala Lys Ala	Gln Lys Met Leu Lys	Glu Leu Ile Thr Ser	Thr
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Arg Leu Gly Thr	Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe	Gly
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Glu Gly Pro Leu	Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile	Pro
	140	145	150
Glu His Arg Arg	Leu Met Leu Ser Pro	Glu Val Val Gln Ala	Leu
	155	160	165
Leu Val Glu Glu	Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala	Val
	170	175	180
Pro Tyr Arg Ala	Glu Tyr Glu Val Asp	Pro Glu Gly Leu Val	Ile
	185	190	195
Leu Glu Ala Ser	Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr	Leu
	200	205	210
Gly Cys Tyr Arg	Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu	Arg
	215	220	225
Leu Lys Gly Pro	Asp His Leu Ala Ser	Ser Cys Leu Trp His	Leu
	230	235	240
Gln Gly Pro Lys	Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp	Thr
	245	250	255
Leu Ala Glu Cys	Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala	Gly
	260	265	270
Pro Leu Glu Lys	Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser	Arg
	275	280	285
Gln Glu Pro Val	Val Glu Val Leu Ala	Ser Gly Ala Ile Met	Ala
	290	295	300
Val Val Trp Lys	Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe	Val
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Leu Ser Val Gln	Pro Val Val Phe Gln	Ala Cys Glu Val Asn	Leu
	320	325	330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr	Pro
	335	340	345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp	His
	350	355	360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe	Asp
	365	370	375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr	Gln

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Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly					
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Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro					
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Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met					
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Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln					
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Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu					
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Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val					
				650					655					660					
Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val					

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Leu His Cys Trp Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser	
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<210> 170

<211> 1327

<212> DNA

<213> Homo sapiens

<400> 170

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

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<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

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<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

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aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
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His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
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Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
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Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
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Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
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Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
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Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
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Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
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Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
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Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
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Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg
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Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg
335 340 345

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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

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<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 180

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<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 181

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<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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ctggtgccac agcctgctac ctgcctgctg accgctgcaa ctaccagact 1700
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caatttccga tgccgggacg agaagtgcgt gtatgagacg tgggtgtgcg 1800
atgggcagcc agactgtgcg gacggcagtg atgagtggga ctgctcctat 1850
gttctgcccc gcaaggtcat tacagctgca gtcattggca gcctagtgtg 1900
cggcctgctc ctggtcatcg ccctgggctg cacctgcaag ctctatgcca 1950
ttcgcaccca ggagtacagc atctttgcc ccctctccc gatggaggct 2000
gagattgtgc agcagcaggc accccttcc tacgggcagc tcattgcca 2050
gggtgccatc ccacctgtag aagacttcc tacagagaat cctaataata 2100
actcagtgtg gggcaacctg cgttctctgc tacagatctt acgccaggat 2150
atgactccag gaggtggccc aggtgcccgc cgtcgtcagc ggggccgctt 2200
gatgcgacgc ctggtacgcc gtctccgccg ctggggcttg ctccctcgaa 2250
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gaagccccag ggccactgcc ctcaactgcc ctagagccat cactattgtc 2500
tggagtgggtg caggccctgc gagggcgctt gttgccagc ctggggcccc 2550
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gaagatgagg acgatgtgct actgggtgcca ctggctgagc cgggggtgtg 2650
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ttcagggact tgggtggcct ccggttgacc ctatgtagct gctataaagt 2850
taagtgtccc tcaggcaggg agagggctca cagagtctcc tctgtacgtg 2900

gccatggcca gacaccccag tcccttcacc accacctgct cccacgcca 2950
 ccaccatttg ggtggctggt tttaaaaagt aaagttctta gaggatcata 3000
 ggtctggaca ctccatcctt gccaaacctc tacccaaaag tggccttaag 3050
 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
 ctcacaaaaa gagtgaaca aatgcttcta ttccatagct acggcattgc 3200
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183
 <211> 713
 <212> PRT
 <213> Homo sapiens

<400> 183
 Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Gly Gly Ala Leu
 1 5 10 15
 Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp
 20 25 30
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro
 35 40 45
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu
 50 55 60
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys
 65 70 75
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro
 80 85 90
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu
 95 100 105
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly
 110 115 120
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln
 125 130 135
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His
 140 145 150
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys
 155 160 165
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro
 170 175 180
 Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr

185										190					195				
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His					
				200					205					210					
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp					
				215					220					225					
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp					
				230					235					240					
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro					
				245					250					255					
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn					
				260					265					270					
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val					
				275					280					285					
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala					
				290					295					300					
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys					
				305					310					315					
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg					
				320					325					330					
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala					
				335					340					345					
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His					
				350					355					360					
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr					
				365					370					375					
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly					
				380					385					390					
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg					
				395					400					405					
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly					
				410					415					420					
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr					
				425					430					435					
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu					
				440					445					450					
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys					
				455					460					465					
Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu					

470										475					480				
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser					
				485					490					495					
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp					
				500					505					510					
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu					
				515					520					525					
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly					
				530					535					540					
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg					
				545					550					555					
Leu	Val	Arg	Arg	Leu	Arg	Arg	Trp	Gly	Leu	Leu	Pro	Arg	Thr	Asn					
				560					565					570					
Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser					
				575					580					585					
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg					
				590					595					600					
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro					
				605					610					615					
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala					
				620					625					630					
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro					
				635					640					645					
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly					
				650					655					660					
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro					
				665					670					675					
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp					
				680					685					690					
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu					
				695					700					705					
Ala	Glu	Asp	Glu	Pro	Leu	Leu	Thr												
				710															

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcttgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150
 aataaaacat cgcccccttct gcttcagtgt gaaagggcac gtgaagatgc 200
 tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcactgga tttgaagtca cggttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450
 agttgggtgga ggggtgtttg cacttgtagc agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
 cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
 ttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe	15
1				5					10						
Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val	30
				20					25						
Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr	45
				35					40						
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile	60
				50					55						
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe	75
				65					70						
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe	90
				80					85						
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr	105
				95					100						
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys	120
				110					115						
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn	135
				125					130						

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
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ttttgcagaa octactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggg aacaacagta ttcattgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgccggccga gtcgctgagc cgcggtgcc ggacgggacg 50
ggaccggcta ggctgggcgc gccccccggg ccccgccgtg ggcatgggcg 100
cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150
gccgccccgc agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200
cgcgccacg aaccgcgtag ttgcgcccac cccgggaccc gggaccctg 250
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300
tccccgcgg gcgcgcgcaa cttcttggcc atggtagaca acctgcaggg 350
ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400
agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450
ggaacccccgc actcctacat agacacgtac ttgacacag agaggtctag 500
cacataccgc tccaagggtt ttgacgtcac agtgaagtac acacaaggaa 550
gctggacggg cttcgttggg gaagacctcg tcaccatccc caaaggcttc 600
aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700
cacttgccaa gccatcaagt tctctggaga ccttcttcga ctccctggtg 750
acacaagcaa acatccccaa cgttttctcc atgcagatgt gtggagccgg 800
cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850
gaattgaacc aagtttgat aaaggagaca tctggtatac ccctattaag 900
gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
acagtggcac cacgctgctg cgctgcccc agaagggtgtt tgatgcggtg 1050
gtggaagctg tggcccgcgc atctctgatt ccagaattct ctgatgggtt 1100
ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttgg 1150
cttacttccc taaaatctcc atctacctga gagacgagaa ctccagcagg 1200
tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1250
ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa 1300
atgcgctggt gatcggtgcc acgggtgatgg agggcttcta cgtcatcttc 1350
gacagagccc agaagagggt gggcttcgca gcgagcccct gtgcagaaat 1400
tgcaggtgct gcagtgtctg aaatttccgg gccttttcta acagaggatg 1450
tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc cattttgtgg 1500
attgtgtcct atgcgctcat gagcgtctgt ggagccatcc tccttgtctt 1550
aatcgtcctg ctgctgctgc cgttccggtg tcagcgtcgc ccccgtagcc 1600
ctgaggtcgt caatgatgag tcctctctgg tcagacatcg ctggaaatga 1650
atagccaggc ctgacctcaa gcaaccatga actcagctat taagaaaatc 1700
acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750
caccgctctt caatctctgt tctgctccca gatgccttct agattcactg 1800
tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850
aaataattaa aaaaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

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Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
				20					25					30

Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
				35					40					45

Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
				50					55					60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala				65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg				80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu				95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly				110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser				125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr				140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile				155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile				170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly				185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser				200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro				215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala				230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu				245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu				260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly				275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala				290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val				305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro				320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp				335	340	345

Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	
				395					400					405	
Val	Ile	Gly	Ala	Thr	Val	Met	Glu	Gly	Phe	Tyr	Val	Ile	Phe	Asp	
				410					415					420	
Arg	Ala	Gln	Lys	Arg	Val	Gly	Phe	Ala	Ala	Ser	Pro	Cys	Ala	Glu	
				425					430					435	
Ile	Ala	Gly	Ala	Ala	Val	Ser	Glu	Ile	Ser	Gly	Pro	Phe	Ser	Thr	
				440					445					450	
Glu	Asp	Val	Ala	Ser	Asn	Cys	Val	Pro	Ala	Gln	Ser	Leu	Ser	Glu	
				455					460					465	
Pro	Ile	Leu	Trp	Ile	Val	Ser	Tyr	Ala	Leu	Met	Ser	Val	Cys	Gly	
				470					475					480	
Ala	Ile	Leu	Leu	Val	Leu	Ile	Val	Leu	Leu	Leu	Leu	Pro	Phe	Arg	
				485					490					495	
Cys	Gln	Arg	Arg	Pro	Arg	Asp	Pro	Glu	Val	Val	Asn	Asp	Glu	Ser	
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Ser	Leu	Val	Arg	His	Arg	Trp	Lys								
				515											

<210> 197
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 197
 cgcaagaagct acagattctc g 21

<210> 198
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 198
 ggaaattgga ggccaaagc 19

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 199
ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggctc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 205
<211> 1939
<212> DNA
<213> Homo sapiens

<400> 205
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<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
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Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
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Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile	80	85	90
Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe	95	100	105
Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile	110	115	120
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe	125	130	135
Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr	140	145	150
His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val	155	160	165
Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe	170	175	180
Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg	185	190	195
Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu	200	205	210
Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala	215	220	225
His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro	230	235	240
Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu	245	250	255
Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu	260	265	270
Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys	275	280	285
His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala	290	295	300
His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro	305	310	315
Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser	320	325	330
Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr	335	340	345
Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
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Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttggacttgg ccag 24

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac ggttgacat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

<400> 210

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acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150

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<210> 211
 <211> 985
 <212> PRT
 <213> Homo sapiens

<400> 211
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 20 25 30
 Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu
 35 40 45
 Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu
 50 55 60
 Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly
 65 70 75
 His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
 80 85 90
 Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly
 95 100 105
 Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln
 110 115 120
 Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu
 125 130 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu	530	535	540
Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp	545	550	555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser	560	565	570
Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu	575	580	585
Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp	590	595	600
Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu	605	610	615
Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln	620	625	630
His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu	635	640	645
Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser	650	655	660
Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala	665	670	675
Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg	680	685	690
His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr	695	700	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 212
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<210> 213
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 213
actgaccttc cagctgagcc acac 24

<210> 214
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

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 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
1				5				10					15	

Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
				20					25				30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35					40				45	

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met					
				65					70					75					
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu					
				80					85					90					
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr					
				95					100					105					
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile					
				110					115					120					
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser					
				125					130					135					
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala					
				140					145					150					
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu					
				155					160					165					
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu					
				170					175					180					
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr					
				185					190					195					
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro					
				200					205					210					
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala					
				215					220					225					
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg					
				230					235					240					
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu					
				245					250					255					
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His					
				260					265					270					
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln					
				275					280					285					
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys					
				290					295					300					
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro					
				305					310					315					
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val					
				320					325					330					
Ser	Ala																		

<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
ctgtcttccc ctgcttggct gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
ggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100
cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150
tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggggc tccacctctg 350
ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400

gctgggatca tggtgttggc cctggtctgt ctgctcagct gcctgctacc 450
 ctccagttag gccaaactct acggtcgttg tgaactggcc agagtgtac 500
 atgacttcgg gctggacgga taccgggat acagcctggc tgactgggtc 550
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
 ggtgcagcaa cctcaccccg aacgtcccca acgtgtgccg gatgtactgc 700
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctggggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15

Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75

Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140					145	

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tggtggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
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gtgcctgcgt tcgctgcgcc tcctcgtctt cgcggtcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaagtgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctccggtgcgc cgcggtgccc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctcttc ggcaaggtgg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400
ttgcagtgac gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500
ctctgacaac atcgccctacg gtgtggcctt ctcacagtcg tttgtggatg 550
tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc cacgggggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttccgc cagggtgggtc acgcactgaa ggagaagttt 750
gatggtgcca ctgagggtgga gccacgccgc gtgggctcct ccagggcact 800
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900
ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950
ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg cagggtggagc 1000
tggtgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050
cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100
ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150
aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200
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caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300
ctgccactga ccaaagggac cttgctcgtg ccgctggctg cccgcatgtg 1350
gctgccactg accactcagt tggtatctgt gtccgttttt ctacttgag 1400
acctaaagtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450
gtcatcgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500
atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550
tacacatgga ctctggcag cttgagccta gaagccatgt ctctcaaagt 1600
ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650
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gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750
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agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccg 1850

gctgtgcctt tgcagtcac cccgagtcac ctttcacagc gctgttcctc 1900
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
acacacacac ggacacacac acacacctgc gagagagagg gaggaaagg 2000
ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
<211> 351
<212> PRT
<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe	1	5	10	15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys	20	25	30	
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys	35	40	45	
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn	50	55	60	
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile	65	70	75	
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser	80	85	90	
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly	95	100	105	
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val	110	115	120	
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys	125	130	135	
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe	140	145	150	
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe	155	160	165	
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser	170	175	180	
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg	185	190	195	
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly	200	205	210	
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro				

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 227
 gctgcagctg caaattccac tgg 23

<210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 228
 tgggtgggaga ctgttttaa ttcggcc 28

<210> 229
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggctccacg gagcgcgcgg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
gcggcgcgtg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
cgcgtgaccc agggcttggc tgaagccggc aggggccgtg aggacgtccg 500
cactgagctg ttccgggcgc tggaggccgt gaggctccag aacaactcct 550
gcgagccgtg cccacgctc tggctgtcct tcgagggtc ctgctacttt 600
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650
tgccagcgcg cacctgggtga tcgttggggg cctggatgag cagggttcc 700
tcaactcgaa cacgcgtggc cgtggttact ggctgggcct gagggtgtg 750
cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
ccgcccagtg ccctggagcc gcgccattg cagcatgtcg tatcctgggg 1000
gctgctcacc tccctggctc ctggagctga ttgccaaaga gttttttct 1050
tctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100
tgtccagccc agtgccctggg ctctgggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
 ctctcgcgtc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250
 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
 aaaaa 1355

<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu	1	5	10	15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg	20	25	30	
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp	35	40	45	
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg	50	55	60	
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser	65	70	75	
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp	80	85	90	
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr	95	100	105	
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu	110	115	120	
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala	125	130	135	
Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	140	145	150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	155	160	165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	170	175	180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	185	190	195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	200	205	210	

Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu
				215					220					225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val
				230					235					240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro
				245					250					255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr
				260					265					270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp
				275					280					285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys							
				290										

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gagggatgac cgacccgggg aaggtcgctg ggcagggcga 50
gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100
ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150
agacaggagg aactggagcc tcattggccg gccggggcg cgggcctcgg 200
gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250
cgctcccgt gctcctgccg ggtgatggaa aacccagcc cggccgccgc 300
cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgcgcgcg 350
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400
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cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550
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cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700
cagcgcaggc actcgctggt ctcgtttggt gtgcgcatcg tgcccagccc 750
cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800
ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850
agcggcttca ccttctctc ccccaacttc gccaccatcc cgcaggacac 900
ggtgaccgag ataacgtcct cctctcccag ccaccggcc aactccttct 950
actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000
cggctgcgac agagccccag ggccttcac cctcccgccc cagtccctgcc 1050
cagcagggac aatgagattg tagacagcgc ctcaattcca gaaacgccgc 1100
tggactgcga ggtctccctg tggctgtcct ggggactgtg cggaggccac 1150
tgtgggaggc tcgggaccaa gagcaggact cgctacgtcc ggggccagcc 1200
cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250
tccctgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggcccc 1300
cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1350
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cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
 aaacagcctc ctcccttccc aaccttgctt cttagggggc cccgtgtccc 1500
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 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys	1	5	10	15
Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly		20	25	30	
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile		35	40	45	
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr		50	55	60	
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala		65	70	75	
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val		80	85	90	
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala		95	100	105	
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val		110	115	120	
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln		125	130	135	
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser		140	145	150	
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val		155	160	165	

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala	170	175	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe	185	190	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val	200	205	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	215	220	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr	230	235	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala	245	250	255
Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser	260	265	270
Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser	275	280	285
Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser	290	295	300
Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro	305	310	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys	320	325	330

Val

<210> 237
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 237
 cagcactgcc aggggaagag gg 22

<210> 238
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 238
 caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagccccttc tcctcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtcctgcggg atg 23

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894
<212> DNA
<213> Homo sapiens

<400> 244

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aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300
cagaaatfff atccaactff gtttggaagc ttattatgac aataccatff 350
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acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaattg 500
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
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 ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450
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 catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550
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 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800
 catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 245
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val
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 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
 20 25 30
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
 35 40 45
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
 50 55 60
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
 65 70 75
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
 80 85 90
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
 95 100 105
 Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala
 110 115 120
 Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly
 125 130 135

Asp Thr Val Tyr	Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu	Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu	Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
455 460 465

Arg Glu Lys Lys Glu Arg Arg
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tggtgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
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 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
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 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
 35 40 45
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
 50 55 60
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
 65 70 75
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
 80 85 90
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 95 100 105
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
 110 115 120
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
 125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro
425 430 435

Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu
440 445 450

Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn
455 460 465

Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp
470 475 480

Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met
485 490 495

Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr
500 505 510

Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala
515 520 525

Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu
530 535 540

Pro Gln Glu Trp Ala
545

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

agggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257
gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258
<211> 2764
<212> DNA
<213> Homo sapiens

<400> 258
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ggagattctg gatacgagtg caggagtacg tgatgggtgcc ggagggcctg 150
tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250
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cttggtgatc agagacgcg agatgcagga tgagtcacag tacttctttc 400
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caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550
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gcctgtaatc ccagcacttt gggaggttga ggtgggcaga tcgcctgagg 1900
tcgggagttc gagaccagcc tggccaactt ggtgaaaccc cgtctctact 1950
aaaaatacaa aaattagctg ggcattggtg caggcgcctg taatcctacc 2000
tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050
tgcagtgagc caagatcaca ccattgcacg ccagcctggg caacaaagcg 2100
agactccatc tcaaaaaaaaa aatcctcaa atgggttggg tgtctgtaat 2150
cccagcactt tgggaggcta aggtgggtgg attgcttgag cccaggagtt 2200
cgagaccagc ctgggcaaca tggtgaaacc ccatctctac aaaaaataca 2250
aaacatagct gggcttgggtg gtgtgtgcct gtagtcccag ctgtcagaca 2300
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agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700
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 tcaccttaaa aaaa 2764

<210> 259
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 259

Met	Leu	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Gly	Gly	Ser	Gln	1	5	10	15
Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met	20	25	30	
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp	50	55	60	
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr	65	70	75	
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe	80	85	90	
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile	95	100	105	
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val	110	115	120	
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe	125	130	135	
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp	140	145	150	
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly	155	160	165	
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro	170	175	180	
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu	185	190	195	
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys	200	205	210	
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro	215	220	225	

Ala Thr Leu Ser	Trp Val Leu Gln Asn Arg	Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly	Pro Arg Pro Leu Gly	Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp	Ser Gly Arg Tyr Thr	Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln	Gln Arg Ala Leu Asp	Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu	Arg Val Met Val Ser	Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu	Gly Asn Gly Thr Ser	Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys	Leu Val Cys Val Thr	His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp	Thr Gln Arg Gly Gln	Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro	Gly Val Leu Glu Leu	Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu	Phe Thr Cys His Ala	Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser	Leu Ser Leu Ser Val	His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala	Phe Ser Asn Gly Ala	Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu	Phe Leu Cys Leu Ala	Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg	Arg Thr Gln Thr Glu	Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser	Thr Ile Leu Asp Tyr	Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu	Ala Gln Lys Arg Asn	Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr	Pro Pro Pro Pro Gly	Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln	Lys Lys Gln Tyr Gln	Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser	Thr Gln Ala Pro Glu	Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 260
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 260
caaagcctgc gcctggtctg tg 22

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 261
ttctggagcc cagagggtgc tgag 24

<210> 262
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
ggagctgcc cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
<211> 2857
<212> DNA
<213> Homo sapiens

<400> 263
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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100
caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150
ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450
tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
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tcactacaag taactcactg gatcgtgaaa tcagtgttg gtacaaccta 1350
agtattacag ccacagaaaa atacaatata gaacagatct cttogatccc 1400
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 ttccaatatg atgatgaagg ggggtggagaa gaagatacag aggcctttga 2000
 tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050
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<210> 264
 <211> 772
 <212> PRT
 <213> Homo sapiens
 <400> 264

Met	Asn	Cys	Tyr	Leu	Leu	Leu	Arg	Phe	Met	Leu	Gly	Ile	Pro	Leu	1	5	10	15
Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys	20	25	30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	35	40	45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	50	55	60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	65	70	75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	80	85	90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	95	100	105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	110	115	120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	125	130	135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	140	145	150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	155	160	165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	170	175	180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	185	190	195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	200	205	210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	215	220	225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	230	235	240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	245	250	255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	260	265	270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	275	280	285	

Gly Glu Asn Ala	Glu Met Asp Tyr Ser	Ile Glu Glu Asp Asp Ser	290	295	300
Gln Thr Phe Asp	Ile Ile Thr Asn His	Glu Thr Gln Glu Gly Ile	305	310	315
Val Ile Leu Lys	Lys Lys Val Asp Phe	Glu His Gln Asn His Tyr	320	325	330
Gly Ile Arg Ala	Lys Val Lys Asn His	His Val Pro Glu Gln Leu	335	340	345
Met Lys Tyr His	Thr Glu Ala Ser Thr	Thr Phe Ile Lys Ile Gln	350	355	360
Val Glu Asp Val	Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr Tyr	365	370	375
Val Phe Glu Val	Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val Gly	380	385	390
Val Val Ser Ala	Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile Arg	395	400	405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn Gly	410	415	420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala Trp	425	430	435
Tyr Asn Leu Ser	Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu Gln	440	445	450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn Asp	455	460	465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys Glu	470	475	480
Asn Ala Gly Ser	Gly Gln Val Ile Gln	Thr Ile Ser Ala Val Asp	485	490	495
Arg Asp Glu Ser	Ile Glu Glu His His	Phe Tyr Phe Asn Leu Ser	500	505	510
Val Glu Asp Thr	Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn Gln	515	520	525
Asp Asn Thr Ala	Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn Leu	530	535	540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp Asn	545	550	555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn	Thr Leu Thr Ile His Val	560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	575	580	585
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	590	595	600
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	605	610	615
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	620	625	630
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	635	640	645
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg cacc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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cccgcccttaa cttcctccgc ggggcccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ccttctgcac ctgccacccc tgagccagcg 200
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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
				125					130					135					
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr					
				200					205					210					

Val

<210> 271

<211> 564

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 21, 69, 163, 434, 436, 444

<223> unknown base

<400> 271

ttctggccaa acccggggct ncagctgttg ggcttcatct cgccttcctg 50

ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100

ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
tgatgggtggg tggcatcctc ctgggagtga tagcaatctt tgtggceacc 300
gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450
gaccctatga cccagtgcaa tgccaggtag gaatttggc aggctctctt 500
cactggctgg gctgctgctt ctctctgcct totgggaggt gccctacttt 550
gctgttcttg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50
tccagctggt gggcttcatt ctccccttcc tgggatggac cggcgcccac 100
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtccctgcgtg 200
tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250
atctgagcag cacattgcaa gcaaccctg ccttgatggg ggttggcatc 300
ctcctgggag tgatagcaat cttnntggcc accgttgtnn ntgaagtgt 350
tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgcga tatttcttct tgcaggtctg gctattttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273

gggcccgcacc attatccaac cgggntcact gttggctcat ctccctcctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccctat 100
gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac cntgccctg atggtggttg 250
gcatcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttggaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450
cccagtcaat gccaggtagc aatttggtca ggctctcttc actggctggg 500
ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctcccct cctggatgga tcgcnccacc gtcacattgc cttcccccan 50
tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100
ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
caaccctgac cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
ttgtggccac cgttggcatg aagtgtatga agtgcttgga agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400
cnnngnnntct atgaccctat gaccccagtc aatgccaggt acgaatttgg 450

tcaggctctc ttcaactggct gggctgctgc ttctctctgc cttctgggag 500
gtgccctact ttgctgttcc tgtccc 526

<210> 275
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
<223> unknown base

<400> 275
agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50
gcagcacatt ncaagcaacc ccttgccttg aagggtggtg ncatcccccc 100
tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200
gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300
tgccaggtag gaatttggtc aggtctctct cactggctgg gctgctgctt 350
ctctctgcct tctgggaggt gccctacttt gctgttctctg tccccgaa 398

<210> 276
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
<223> unknown base

<400> 276
agcaatgccc tgccccaggt ggaggattaa ttcctatgnt ggggacaaca 50
ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100
cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150
gagcagcaca ttgcaagcaa cccgtgcctt gatggtgggt ggcatcttcc 200
tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300
cgcgatattt cttnttgacg gtctggctat tttagttgcc acagcatggt 350
atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttggcca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50

cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttggtc aggctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

ttcctgggat ggatccgccc ccattntcac atgccctgcc ccttgagat 50

ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150

aagtctttga ctcttgctg aatctgagca gcacattgca agcaaccntg 200

ccttgatggg ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgtg tgaagtgtt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgca tatttcttct tgcaggctctg 350

gctatttttag nngccacagc atggatatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgaccca gtcaatgcc ggtacgaatt tggtcaggct 450

ctcttcaactg gctgggctgc tgcttctctc tgccttctgg gaggtgcct 500

actttgctgt tcctgtcccc gaaaaacaac ctcttaccca cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctgttgggc ttcattctgc ttcctgggat ggaatcggcg 50
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gaccnccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200
aatctgagca gcacattgca agcaaccntg ccttgatggg ggttggcatc 250
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350
ggggcgcgat atttcttctt gcaggctctg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcaactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttgcgtgt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctcgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gcgtgccgtc agctcgccgg gcaccgcggc ctgccctcg ccctccgccc 50

ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccaccccg 100

tagaggaccc ccgcccgtgc ccgaccgggt ccccgctttt ttgtaaaact 150

taaagcgggc gcagcattaa cgcttccgcg cccggtgacc tctcaggggt 200

ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250

ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300

ccgatgttgt caccaccaac ctaaagcttg gcaaccgcac agaccgaaat 350

gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400

caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450

tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500

gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550

gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600

ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650

attatatcca caactgcata aaagacagaa acaccaatag tgtctaagtc 700

tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750

gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800

ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850

ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcaccc 900

ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950

aagattgcct tgtagaggta gcatgcacag gatggtaaat tggattggtg 1000

gatccacat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgccttttaa ttacccctcc 1100
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200
ctttattaat gacaaggga accatgagta atgccacaat ggcatattgt 1250
aatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
tctcttaaaa tgacaccctt cctcgctgtg tgggtgctggc ccttggggag 1350
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acgtggccca ctcgccggcc aggtgctttt ccgtgtcttc agttctgtcc 1450
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taaagggacc aagctaaatt tgtattgggt catgtagtga agtcaaactg 1650
ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatt 1700
catgttttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750
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ctctggagag tctggatcag tggaggtggg gtttattggg atgctggaga 1850
agagctgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900
gggagggaaa ttctcagtag tgacagtcaa ctctagggtt ctttttttaa 1950
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
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gagagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

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Leu Lys Phe Arg Gly	Pro Phe Thr Asp	Val Val Thr Thr Asn	Leu
20		25	30
Lys Leu Gly Asn Pro	Thr Asp Arg Asn	Val Cys Phe Lys	Val Lys
35		40	45
Thr Thr Ala Pro Arg	Arg Tyr Cys Val	Arg Pro Asn Ser	Gly Ile
50		55	60
Ile Asp Ala Gly Ala	Ser Ile Asn Val	Ser Val Met Leu	Gln Pro
65		70	75
Phe Asp Tyr Asp Pro	Asn Glu Lys Ser	Lys His Lys Phe	Met Val
80		85	90
Gln Ser Met Phe Ala	Pro Thr Asp Thr	Ser Asp Met Glu	Ala Val
95		100	105
Trp Lys Glu Ala Lys	Pro Glu Asp Leu	Met Asp Ser Lys	Leu Arg
110		115	120
Cys Val Phe Glu Leu	Pro Ala Glu Asn	Asp Lys Pro His	Asp Val
125		130	135
Glu Ile Asn Lys Ile	Ile Ser Thr Thr	Ala Ser Lys Thr	Glu Thr
140		145	150
Pro Ile Val Ser Lys	Ser Leu Ser Ser	Ser Leu Asp Asp	Thr Glu
155		160	165
Val Lys Lys Val Met	Glu Glu Cys Lys	Arg Leu Gln Gly	Glu Val
170		175	180
Gln Arg Leu Arg Glu	Glu Asn Lys Gln	Phe Lys Glu Glu	Asp Gly
185		190	195
Leu Arg Met Arg Lys	Thr Val Gln Ser	Asn Ser Pro Ile	Ser Ala
200		205	210
Leu Ala Pro Thr Gly	Lys Glu Glu Gly	Leu Ser Thr Arg	Leu Leu
215		220	225
Ala Leu Val Val Leu	Phe Phe Ile Val	Gly Val Ile Ile	Gly Lys
230		235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

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tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggnga gagaaactct tcagcgaatc 200
cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50
gattacctcc ttaaattgaca cnttcctcg cctgttggtg ctggccnttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242
<223> unknown base

<400> 287
ccctggtggt ttgtttcttt aattcgttgg tgtaattntt gggaagattg 50
cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggatttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351
<223> unknown base

<400> 288
ggtggcccat tcccggccca ggctgctttc cggtnttcag ttctgtccaa 50
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgcctt tgttcantta 200
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
ntgttggggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
<211> 320
<212> DNA
<213> Homo sapiens

<400> 289
tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
gaaataaatg gcagtgccttt gttcacttaa agggaccaag ctaaatttgt 200
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
gaaacntgn gtaatgccac aatggcatat tgtaaatgtc attttaaaca 100
ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200
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cccaggctgc tttccgtgct ttcagttctg tccaagccat cagctccttg 300
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550
acaagggtag agttaatgct gcgtgctgct gaantctgtt ggggtgaantg 600
gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50
cacagtagtc cccacgtggc ccaactcccgg cccaggetgc tttccgtgtc 100
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
gagaggcgtg tgttgactga ttgacccagc gctttggaaa taaatggcag 250
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tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
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<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50
ggctggctga gaggtccca gctgcagcgt ccccgccgc ctctcggga 100
gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150
gtctcacttt gttgcccagg ctggagttca gtgccatgat catgggttac 200
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300
atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350
attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400
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tacagtgtgt ggcatcgaat gccagaaaaga actcccaact ccagccttt 500
ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550
cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600
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 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
 atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
 ttcagctcat gccctcaatg tttatattgt gttatctgtt gggctctggga 2050
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 attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
 caatgtgtat tatttaaaaaa tgggagaaat agtttggtct atgaaataaa 2200
 cctagtttag aaatagggaa gctgagacat tttaagatct caagttttta 2250
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 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
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 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
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Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20										25					30				
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu					
				35					40					45					
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr					
				50					55					60					
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu					
				65					70					75					
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn					
				80					85					90					
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu					
				95					100					105					
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg					
				110					115					120					
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp					
				125					130					135					
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu					
				140					145					150					
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu					
				155					160					165					
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly					
				170					175					180					
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser					
				185					190					195					
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala					
				200					205					210					
Ser	Gly	Gly	Asp	Gln	Arg	Glu	Gly	Thr	Arg	Glu	His	Leu	Gln	Glu					
				215					220					225					
Arg	Ala	Lys	Gly	Gly	Arg	Arg	Arg	Lys	Lys	Ser	Gly	Arg	Gly	Gln					
				230					235					240					
Arg	Ile	Ala	Glu	Gly	Arg	Pro	Ser	Phe	Gln	Trp	Thr	Arg	Val	Lys					
				245					250					255					
Asn	Thr	His	Ile	Pro	Lys	Gly	Trp	Ala	Arg	Gly	Gly	Met	Gly	Asp					
				260					265					270					
Ala	Thr	Leu	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Arg	Ala					
				275					280					285					
His	Lys	Lys	Lys	Tyr	Met	Glu	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Lys					
				290					295					300					
Lys	Met	Pro	Gly	Gly	Met	Ile	His	Phe	Ser	Gly	Phe	Asp	Asn	Asp					

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu		
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser		
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys		
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp		
365	370	375
Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg		
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly		
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcgttccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaagggaggc cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300

<211> 1869

<212> DNA

<213> Homo sapiens

<400> 300

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ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcttgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccattggag tgaatgctca cgcacctgcg ggggaggggc ctcctactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400
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gaatggcttc ctgtgtctaa tgacctgac aacccatgtt cactcaagtg 500
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggtcttag 550
atggtacgcg ttgctataca gaatctttgg atatgtgcat cagtggttta 600
tgccaaattg ttggctgcca tcaccagctg ggaagcaccg tcaaggaaga 650
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctgggtccgag 700
ggcagtataa atcccagctc tccgcaacca aatcggatga tactgtgggt 750
gcattccct atggaagtag acatattcgc cttgtcttaa aaggtcctga 800
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cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
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agttcatctt ctatcaaccc atcatccacc gatggaggga gacggatttc 1050
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 gtttaaagaa agcagtgctt cactggttgt agctttcatg ggttctgaac 1800
 taagtgtaat catctacca aagctttttg gctctcaa 1850
 ttagtttcaa aaaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
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 ctgggcgggg cgctgtggct ggcgggccgc cggttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
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 gctccaggaa gaggctaggc tggatgtctt gatcaataac gcagggatct 500
 tccagtggcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
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 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcacccgtc aatgtgttgc 800
 atcctggtat tgtacggaca aatctgggga ggcacatata cattccactg 850
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 cccaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
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 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
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 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
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 agagggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
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 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly	1	5	10	15
Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln	20	25	30	
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr	35	40	45	
Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	50	55	60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	65	70	75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	80	85	90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly				

	95	100	105
Val Gly Glu Leu	Ile Val Arg Glu Leu	Asp Leu Ala Ser Leu	Arg
	110	115	120
Ser Val Arg Ala	Phe Cys Gln Glu Met	Leu Gln Glu Glu	Pro Arg
	125	130	135
Leu Asp Val Leu	Ile Asn Asn Ala Gly	Ile Phe Gln Cys Pro	Tyr
	140	145	150
Met Lys Thr Glu	Asp Gly Phe Glu Met	Gln Phe Gly Val Asn	His
	155	160	165
Leu Gly His Phe	Leu Leu Thr Asn Leu	Leu Leu Gly Leu Leu	Lys
	170	175	180
Ser Ser Ala Pro	Ser Arg Ile Val Val	Val Ser Ser Lys Leu	Tyr
	185	190	195
Lys Tyr Gly Asp	Ile Asn Phe Asp Asp	Leu Asn Ser Glu Gln	Ser
	200	205	210
Tyr Asn Lys Ser	Phe Cys Tyr Ser Arg	Ser Lys Leu Ala Asn	Ile
	215	220	225
Leu Phe Thr Arg	Glu Leu Ala Arg Arg	Leu Glu Gly Thr Asn	Val
	230	235	240
Thr Val Asn Val	Leu His Pro Gly Ile	Val Arg Thr Asn Leu	Gly
	245	250	255
Arg His Ile His	Ile Pro Leu Leu Val	Lys Pro Leu Phe Asn	Leu
	260	265	270
Val Ser Trp Ala	Phe Phe Lys Thr Pro	Val Glu Gly Ala Gln	Thr
	275	280	285
Ser Ile Tyr Leu	Ala Ser Ser Pro Glu	Val Glu Gly Val Ser	Gly
	290	295	300
Arg Tyr Phe Gly	Asp Cys Lys Glu Glu	Glu Leu Leu Pro Lys	Ala
	305	310	315
Met Asp Glu Ser	Val Ala Arg Lys Leu	Trp Asp Ile Ser Glu	Val
	320	325	330
Met Val Gly Leu	Leu Lys		
	335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

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gcaagaaaaat tntgggatat cagtgaagtg atgggtngcc tgctaaaata 100
ggaacaagga gtaaaagagc tgtttataaa actgcataatc agttatatct 150
gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccattgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcagggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50

cggagcccag ccctttccta acccaacca acctagccca gtcccagccg 100

ccagcgccctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150

cttccatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 200

gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250

atagatgaaa ttttaacaa tgctgatgtt gctttagtaa atttttatgc 300

tgactgggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350

ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400

agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450

caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500

aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550

caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600

tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650

cggacaacta tagagttttt gaacgagtag cgaatatattt gcatgatgac 700

tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750

tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800

tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850

gataaatgtg ttctctttgt ccgagaaata acatttgaaa atggagagga 900

attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950

atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000

agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100

ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150

ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200

actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc .cacctgagag ctccttccag 1300
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
 gctttaaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
 cctacgtggg ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 309
 Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser
 1 5 10 15
 Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu
 20 25 30
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
 35 40 45
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
 50 55 60
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
 65 70 75
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
 80 85 90
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
 95 100 105
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
 110 115 120
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
 125 130 135
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
 140 145 150
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
 155 160 165
 Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg
 170 175 180
 Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe
 185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 36, 48
 <223> unknown base

 <400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tcgccgngg agcccgggtc 50
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150
ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttaccgacc tcagatgtc cttctgtc ctggttaactt 250
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactgggtg cgtttcagtc agatgtggca tccaatttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttccta tccttaccgc acctcagatg ctcccttctg ctcttg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttgggtga gctcttagaa 450

caacacacag aagaattggc ccagttaagt gcatgcaaaa agccacaaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaaata gtttccacat 600

ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttggg ttcatgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt ctttaagcata agtaaactg atataaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaattgtgt 1150
 ttttatttgt aagacattac ttattaagaa attgggttatt atgcttactg 1200
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5					10					15

Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25					30

Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40					45

Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55					60

Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70					75

Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85					90

Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100					105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323
<211> 477
<212> DNA
<213> Homo sapiens

<400> 323
attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
tgtaataccc tgaatcccct tgtactcca gactacctca tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
atatgccct cttggcatat catatttga ggtatatgag tagaccagtg 200
atgagtggcc caggactcta tgacctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgatc agttacttta aaaaatg 477

<210> 324
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 324
tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 325
caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggacccaact ggggctcccg ccgctgctgc tgetgacat ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttoccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500
 aactctggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
 gttatatcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
 ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
 aactcttgct ctctcgggtga tggatttgct ttggatttgt tgtgcaactg 850
 ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
 ttctcttggt gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
 ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
 ttttaaaatg gtttcatttg atataggcct taagaaatca ctataaaatg 1150
 caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10				15	

Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25				30	

Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40				45	

Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55				60	

Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70				75	

Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85				90	

Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100				105	

Gln Ser Asp Glu Gln Tyr Ala Cys His	Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu	Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu	Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln	Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp	Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala	Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu	Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg	Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu	Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser	Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala	Val Glu Gln Tyr Val Pro	260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp	Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser	Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala	Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile		320		

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50

gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatacg 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
tttctcttaa ctctgggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 47
<223> unknown base

<400> 332
cacactggcc ggatctttta gaggctttg accttgacca agggctcngga 50
aaacagcaac aagctgagct gctgtgacag aggggaacaag atggcggcgc 100
cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150
tgctgaccat ggccttgacc ggaggttcgg ggaccgcttc ggctgaagca 200
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350
gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
ttccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
gatggactcc gc 562

<210> 333
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 333
acaagctgag ctgctgtgac ag 22

<210> 334
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg cgggaggttc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cgggcccgag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100
agggcgacag gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200
gcctcctggg cgccgtgtgg ctgtcagct cgggccacgg agaggagcag 250
cccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggttc tggtaagg 850
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950
 tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
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 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaatggtt 1200
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcattttag aaatatctca agaattatgg attgtgttgg 1350
 ttgttttaaa tgctgtctgt ggggaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaaact 1550
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaactttt tatataaagt tgcttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800
 acaaatttta aagttaata ttgaataaaa ggaggattat caaattaata 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
1				5					10				15	

Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
				20				25					30	

Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp	35	40	45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg	50	55	60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg	65	70	75
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	305	310	315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465

Asn Ile His

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgtttttaag ccacagacaa 50
 ttaaaagacc tttaaactcct ttggcttctg gtcaaggagac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200
 caagatatct tttaacaagag acctggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacacgcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtggtacca ttctngagc gccagattt tcaactnttt 400
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500
tttgctg 507

<210> 339
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 339
aagctgccgg agctgcaatg 20

<210> 340
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 340
ttgctttctta atcctgagcg c 21

<210> 341
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
aaaggaggac tttcgactgc 20

<210> 342
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 342
agagattcat ccactgctcc aagtcg 26

<210> 343
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagaggac agaggccaga 100

ggactttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatggat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg gggggccaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agagggtggt ggcagtgtct ctgaagggtcc ataaaagaaa 550

aaagagaagt gtggttaagg aaaatggtct gtgtggagggt gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtta tgtcaggag tagtcttcat 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgccctgt tggatgcttc 800

attccagcct cagggaagcc tggcacccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950
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cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggg 1050
caagggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
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ggagactctc acttcaaccc aggaggtgga gggtgcggtg agccaagatt 1250
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aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
1				5				10					15	
Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
			20					25					30	
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
			35					40					45	
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
			50					55					60	
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
			65					70					75	
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
			80					85					90	
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
			95					100					105	
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
			110					115					120	

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
cacagttccc caccatcact cntcccatc cttccaactt tatttttagc 50
ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
ggagagggac agaggccaga ggactttctca tactggacag aaaccgatca 150
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
tcccagggcc accagaagct gaatttgat acagtgtctt acaacatgtt 300
gggggtggac agcgatggat gctgggtggc gccccctggg atgggccttc 350
aggcgaccgg aggggggacg tttatcgtg ccctgtaggg gggggcccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
tggtgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
agggacagag gccagaggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaactcccc ttcgtcactc acctgttctt gcccttggtg ttcct 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100
gcttctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttat tttt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250
tgcagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
ccccagcagc tgggtgtcac tcaactgaagg tcctgagtgt gatgtcactg 550
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttaccgac ctgggatgga gatcaccaaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttggtg 750
gcctactgga ggaggagcc tggtgccgag gaacatgtca aaatggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
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ttcagccaga cagaatgtgt ggagggtgcaa ggagaggcca tccccctggt 950
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cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
 gtgggtgggcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100
 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
 ctctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
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 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650
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 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1				5				10					15	

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
			20					25					30	

Glu Val Ala Ile	Leu Pro Ala Pro	Gln Asn Leu Ser	Val Leu Ser
35		40	45
Thr Asn Met Lys	His Leu Leu Met	Trp Ser Pro	Val Ile Ala Pro
50		55	60
Gly Glu Thr Val	Tyr Tyr Ser Val	Glu Tyr Gln Gly	Glu Tyr Glu
65		70	75
Ser Leu Tyr Thr	Ser His Ile Trp	Ile Pro Ser	Ser Trp Cys Ser
80		85	90
Leu Thr Glu Gly	Pro Glu Cys Asp	Val Thr Asp	Asp Ile Thr Ala
95		100	105
Thr Val Pro Tyr	Asn Leu Arg Val	Arg Ala Thr	Leu Gly Ser Gln
110		115	120
Thr Ser Ala Trp	Ser Ile Leu Lys	His Pro Phe	Asn Arg Asn Ser
125		130	135
Thr Ile Leu Thr	Arg Pro Gly Met	Glu Ile Thr	Lys Asp Gly Phe
140		145	150
His Leu Val Ile	Glu Leu Glu Asp	Leu Gly Pro	Gln Phe Glu Phe
155		160	165
Leu Val Ala Tyr	Trp Arg Arg Glu	Pro Gly Ala	Glu Glu His Val
170		175	180
Lys Met Val Arg	Ser Gly Gly Ile	Pro Val His	Leu Glu Thr Met
185		190	195
Glu Pro Gly Ala	Ala Tyr Cys Val	Lys Ala Gln	Thr Phe Val Lys
200		205	210
Ala Ile Gly Arg	Tyr Ser Ala Phe	Ser Gln Thr	Glu Cys Val Glu
215		220	225
Val Gln Gly Glu	Ala Ile Pro Leu	Val Leu Ala	Leu Phe Ala Phe
230		235	240
Val Gly Phe Met	Leu Ile Leu Val	Val Val Pro	Leu Phe Val Trp
245		250	255
Lys Met Gly Arg	Leu Leu Gln Tyr	Ser Cys Cys	Pro Val Val Val
260		265	270
Leu Pro Asp Thr	Leu Lys Ile Thr	Asn Ser Pro	Gln Lys Leu Ile
275		280	285
Ser Cys Arg Arg	Glu Glu Val Asp	Ala Cys Ala	Thr Ala Val Met
290		295	300
Ser Pro Glu Glu	Leu Leu Arg Ala	Trp Ile Ser	
305		310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
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cctttctagc ttctggccg gctctagaac aattcaggct tcgctgcgac 100
tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcttt attttggaag gaaacaatgt tctaggtcaa actgagtcta 200
ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250
tcatgtgggt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
attctgtcga ataccagggg gaggtagaga gcctgtacac gagccacatc 450
tggatcccca gcagctgggtg ctcaactcact gaaggtcctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagca tctgaagca tccctttaat 600
agaaactcaa ccacacctac ccgacctggg atggagatca ccaaagatgg 650
cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
ggcgctgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggcttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgcccacgcg tccgaggagc aagagagaag agagactgaa 50

acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100

ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150

agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200

tgagagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250

agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300

gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350

ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400

aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450

gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500

ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550

gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600

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agctcacatc ggaccagcac ctgacccga ggactggtgg agctacaagg 700

ataatctcca gggaaacttc gtgccagggc ctcttttctg gggcctggtg 750
 aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccgtgga 800
 tgtggagctg aagaggggttc tttatgaccc ctttctgccc ccattaaggc 850
 tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900
 catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950
 tccccctcctt tacagccacc gactcagtga actgcggctg ctgtttggag 1000
 ctgcgcacgg agccggctcg gaacatcaga tcaaccacca gggcttctct 1050
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 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450
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 tgggtgtcccc catggtcgtg gagactcccc ttcgaggatt gcacccgccc 1600
 gtcctaagcc tccccacaag gcgaggggag ttacccttaa aacaaagcta 1650
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
1				5					10					15

Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
			20						25					30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
			35						40					45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
			50						55					60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

tctgctgagg tgcagctcat tcac 24

<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

ggcgctggt tctgcgcgta ctggctgtac ggagcaggag caagaggtcg 50

ccgccagcct ccgccgccga gcctcgttcg tgtccccgcc cctcgctcct 100

gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccaccca actgcaggtc taattttgga cgctttgcct 200

gccattttctt ccaggttgag ggagccgcag aggcggaggc tcgctattc 250

ctgcagtcag caccacgctc gccccggac gctcggtgct caggcccttc 300

gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400

ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450

atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcattg ctagagcaat tccagccatg gtggttccca 550
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 gctatatattt cttagcagtt atttctacag ttaattacat agtcatgatt 2250
 gttctacggt tcatatatta tatggtgctt tgtatatgcc actaataaaa 2300
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 aaatgtattg tgctttgata ctaaaaatct gtaaatggtt agttttggta 2950
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
1				5				10						15

Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20					25					30

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu		35	40	45
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn		50	55	60
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln		65	70	75
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val		80	85	90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp		95	100	105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu		110	115	120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln		125	130	135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His		140	145	150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys		155	160	165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly		170	175	180
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile		185	190	195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly		200	205	210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser		215	220	225
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys		230	235	240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu		245	250	255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His		260	265	270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser		275	280	285
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg		290	295	300
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala		305	310	315

Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr
320	325 330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile
335	340 345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg
350	355 360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile
365	370 375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr
380	385 390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro
395	400 405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg
410	415 420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr
425	430 435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His
440	445 450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro
455	460 465
Val Asp Lys Arg Lys Thr Tyr Ile Ala	Ser Phe Gln Asn Gly Ile
470	475 480
Phe Ser Glu Ser Leu Gln Asn Pro Pro	Gly Gly Lys Ala Phe Arg
485	490 495
Val Phe Ala Val Val	
500	

<210> 364
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 364
 ggacagaatt tgggagcaca ctgg 24

<210> 365
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50
ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100
agagaaagcc gagcagagct ggggtggcgtc tccggggccgc cgctccgacg 150
ggccagcgcc ctccccatgt ccctgctccc acgccgcgcc cctccggtca 200
gcatgaggct cctggcgggcc gcgctgctcc tgctgctgct ggcgctgtac 250
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gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

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cgagggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450
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ataaaatata ttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu
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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala
				20				25					30

Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35				40						45

Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50				55						60

Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65				70						75

Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80				85						90

Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95				100						105

Arg	Arg	Val	Tyr	Glu	Glu
				110	

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300

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tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850

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 agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050
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 taagagactt tgt 3113

<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

Met	Leu	Asn	Ser	Asn	Val	Leu	Leu	Trp	Leu	Thr	Ala	Leu	Ala	Ile
1				5					10					15
Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150

Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser	155	160	165
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu	170	175	180
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly	185	190	195
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly	200	205	210
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu	215	220	225
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly	230	235	240
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly	245	250	255
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser	260	265	270
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu	275	280	285
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile	290	295	300
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met	305	310	315
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln	320	325	330
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile	335	340	345
Asp	Gly	Asp	Val	Ile	Pro	Asp	Asp	Pro	Gln	Ile	Leu	Met	Glu	Gln	350	355	360
Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Ile	Met	Leu	Gly	Val	Asn	Gln	Gly	365	370	375
Glu	Gly	Leu	Lys	Phe	Val	Asp	Gly	Ile	Val	Asp	Asn	Glu	Asp	Gly	380	385	390
Val	Thr	Pro	Asn	Asp	Phe	Asp	Phe	Ser	Val	Ser	Asn	Phe	Val	Asp	395	400	405
Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Thr	Leu	Arg	Glu	Thr	410	415	420
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Lys	Glu	Asn	Pro	Glu	425	430	435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp	710	715	720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr
770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe
785 790 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly
800 805 810

His Ser Thr Thr Arg Val
815

<210> 376
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 376
ggcaagctac ggaaacgtca tcgtg 25

<210> 377
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 377
aacccccgag caaaagatg gtcac 25

<210> 378
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 378
gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379
<211> 2461
<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggacccct tgggtcgtgg cagcagtggc 50
ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100
ttgttggggg ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150
cgagtacttg aaacgggagc actcgtgtc gaagccctac caggggtgtg 200
gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250
accagttata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300
gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg caggtgcact 350
tcaaaatcca tggacaagga aagaagaatc tgcattggga tggcttggca 400
atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaacat 450
ggacaaatth gtggggctgg gagtatttgt agacacctac cccaatgagg 500
agaagcagca agagcgggta tccccctaca tctcagccat ggtgaacaac 550
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gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950
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aagccacca cccagggca atgctgctgt gatgtgcctt tccctgcagt 1300
ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350

caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400
 cagaaggccc ttctacttca gttttgaatc cacaaagaat taaaaactgg 1450
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 cttggagggc ctggaactct gagtctcct atgaacctct gtagcctaaa 2350
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 gccgcgactc tagagtcgac ctgcagtagg gataacaggg taataagctt 2450
 ggccgccatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg
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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20				25					30	

Leu	Leu	Leu	Gly	Ser 35	Gly	Gln	Gly	Pro	Gln 40	Gln	Val	Gly	Ala	Gly 45
Gln	Thr	Phe	Glu	Tyr 50	Leu	Lys	Arg	Glu	His 55	Ser	Leu	Ser	Lys	Pro 60
Tyr	Gln	Gly	Val	Gly 65	Thr	Gly	Ser	Ser	Ser 70	Leu	Trp	Asn	Leu	Met 75
Gly	Asn	Ala	Met	Val 80	Met	Thr	Gln	Tyr	Ile 85	Arg	Leu	Thr	Pro	Asp 90
Met	Gln	Ser	Lys	Gln 95	Gly	Ala	Leu	Trp	Asn 100	Arg	Val	Pro	Cys	Phe 105
Leu	Arg	Asp	Trp	Glu 110	Leu	Gln	Val	His	Phe 115	Lys	Ile	His	Gly	Gln 120
Gly	Lys	Lys	Asn	Leu 125	His	Gly	Asp	Gly	Leu 130	Ala	Ile	Trp	Tyr	Thr 135
Lys	Asp	Arg	Met	Gln 140	Pro	Gly	Pro	Val	Phe 145	Gly	Asn	Met	Asp	Lys 150
Phe	Val	Gly	Leu	Gly 155	Val	Phe	Val	Asp	Thr 160	Tyr	Pro	Asn	Glu	Glu 165
Lys	Gln	Gln	Glu	Arg 170	Val	Phe	Pro	Tyr	Ile 175	Ser	Ala	Met	Val	Asn 180
Asn	Gly	Ser	Leu	Ser 185	Tyr	Asp	His	Glu	Arg 190	Asp	Gly	Arg	Pro	Thr 195
Glu	Leu	Gly	Gly	Cys 200	Thr	Ala	Ile	Val	Arg 205	Asn	Leu	His	Tyr	Asp 210
Thr	Phe	Leu	Val	Ile 215	Arg	Tyr	Val	Lys	Arg 220	His	Leu	Thr	Ile	Met 225
Met	Asp	Ile	Asp	Gly 230	Lys	His	Glu	Trp	Arg 235	Asp	Cys	Ile	Glu	Val 240
Pro	Gly	Val	Arg	Leu 245	Pro	Arg	Gly	Tyr	Tyr 250	Phe	Gly	Thr	Ser	Ser 255
Ile	Thr	Gly	Asp	Leu 260	Ser	Asp	Asn	His	Asp 265	Val	Ile	Ser	Leu	Lys 270
Leu	Phe	Glu	Leu	Thr 275	Val	Glu	Arg	Thr	Pro 280	Glu	Glu	Glu	Lys	Leu 285
His	Arg	Asp	Val	Phe 290	Leu	Pro	Ser	Val	Asp 295	Asn	Met	Lys	Leu	Pro 300
Glu	Met	Thr	Ala	Pro 305	Leu	Pro	Pro	Leu	Ser 310	Gly	Leu	Ala	Leu	Phe 315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

<210> 381

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

ccttggtcg tggcagcagt gg 22

<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

cactctccag gctgcatgct cagg 24

<210> 383

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gtcaaacggt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384

<211> 3150

<212> DNA

<213> Homo sapiens

<400> 384

ccgagccggg cgcgcagcga cggagctggg gccggcctgg gaccatgggc 50

gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100

ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150

tgggggtctgg ctcagaattc ctgcagctgg tgaaaatctg ttttctagaa 200

gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250
ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300
tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350
cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400
caagagtcga aagagaatca tgcccgaccc tgtgacggag cccctgtga 450
cagaccccggt ttatgaagct cttttgtact gcaacatccc cagtgtggcc 500
gagcgcagca tggaaggctca tgccccgcat cattttaagc tgggtctcagt 550
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aaacaaagcg accagaaatt gactgcactc tgggtggctaa caggaaaccg 650
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cagaacggctc agctgctgag ggatatctat ctaaagaaac acaaactcct 850
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gtgttgcaatt tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala
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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25					30

Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40					45

Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55					60

Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75

Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90

Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105

Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120

Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135

Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
				140					145					150

Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160					165

Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180

Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
				185					190					195

Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys Ser Gly Ser	Cys Tyr Cys Pro Val	Arg Asn Gln Tyr Leu Glu
245	250	255
Lys Glu Gln Arg	Arg Gln Tyr Leu Leu Arg	Leu Lys Asn Ser Gln
260	265	270
Leu Glu Lys Thr	Tyr Gly Glu Met Ala Lys	Ile Val Asp Val Pro
275	280	285
Thr Lys Gln Leu	Arg Ala Ala Asn Pro Ile	Asp Ser Met Leu Cys
290	295	300
His Phe Cys His	Asn Val Ser Phe Pro Cys	Thr Arg Asn Gly Cys
305	310	315
Val Asp Met Glu	His Phe Lys Val Ile Lys	Thr His Gln Ile Glu
320	325	330
Asp Glu Arg Glu	Arg Arg Glu Lys Lys Leu	Tyr Phe Gly Tyr Ser
335	340	345
Leu Leu Gly Ala	His Pro Ile Leu Asn Gln	Thr Ile Gly Arg Met
350	355	360
Gln Arg Ala Thr	Glu Gly Arg Lys Glu Glu	Leu Phe Ala Leu Tyr
365	370	375
Ser Ala His Asp	Val Thr Leu Ser Pro Val	Leu Ser Ala Leu Gly
380	385	390
Leu Ser Glu Ala	Arg Phe Pro Arg Phe Ala	Ala Arg Leu Ile Phe
395	400	405
Glu Leu Trp Gln	Asp Arg Glu Lys Pro Ser	Glu His Ser Val Arg
410	415	420
Ile Leu Tyr Asn	Gly Val Asp Val Thr Phe	His Thr Ser Phe Cys
425	430	435
Gln Asp His His	Lys Arg Ser Pro Lys Pro	Met Cys Pro Leu Glu
440	445	450
Asn Leu Val Arg	Phe Val Lys Arg Asp Met	Phe Val Ala Leu Gly
455	460	465
Gly Ser Gly Thr	Asn Tyr Tyr Asp Ala Cys	His Arg Glu Gly Phe
470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386
 ccaagcagct tagagctcca gacc 24

<210> 387
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 387
 ttccctatgc tctgtattgg catgg 25

<210> 388
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 388
 gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
 <211> 3313
 <212> DNA
 <213> Homo sapiens

<400> 389
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<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	

Asp Lys Ala Ala	Gln Val Phe Lys Leu	Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile	Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val	Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu	Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu	Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr	Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn	Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu	Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val	Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala	Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser	Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln	Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val	Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn	Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala	Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu	Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln	Val Lys Val Met Ala	Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser	Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala	Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr
860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu
875 880 885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro
905 910 915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgcg ccaagacgtg 200
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
 aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttcgcagcct 300
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 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30

Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45

Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60

Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	
				80					85					90	
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	
				95					100					105	
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	
				110					115					120	
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	
				125					130					135	
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	
				140					145					150	
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	
				155					160					165	
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	
				170					175					180	
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	
				185					190					195	
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	
				200					205					210	
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	
				215					220					225	
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	
				230					235					240	
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	
				245					250					255	
Ile	Gly	Ser	Lys	Gly											
				260											

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gcc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20						25					30

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45

Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
				50					55					60

Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75

Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
				80					85					90

Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
				95					100					105

Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120

Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
				125					130					135

His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150

Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165

Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180

Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195

Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210

Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu
				215					220					225

Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240

Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255

Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser	Glu Val
275		280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys	Arg
290		295	300
Leu Ala Ala Asn	Asp Leu Gln Gly Cys	Ala Val Ala Thr	Gly Pro
305		310	315
Tyr His Pro Ile	Trp Thr Gly Arg Ala	Thr Asp Glu Glu	Pro Leu
320		325	330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys	Ala Ser
335		340	345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala	Leu Lys
350		355	360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly	Ser Gly
365		370	375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro	Gly Ser
380		385	390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser	Glu Pro
395		400	405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly	Cys Ser
410		415	420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln	Ala Gly
425		430	435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly	Ala Leu
440		445	450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala	Leu Val
455		460	465
Leu Trp Thr Val	Leu Gly Pro Cys		
470			

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100

agcctcagat actgggggact ttacagtccc acagaaccgt cctcccagga 150

agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgca 200

caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gaggggaattc 350

tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400

gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450

aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500

ctagagagtc ctttcgagtt ttttcaagct gagctgcaag taatagacat 550

aaacgaccac tctccagtat ttctggacaa acaaatgttg gtgaaagtat 600

cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650

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<210> 405
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 405
 Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu
 1 5 10 15
 Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu
 20 25 30
 Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe
 35 40 45
 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe
 50 55 60
 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His
 65 70 75
 Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys
 80 85 90
 Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu
 95 100 105
 Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala
 110 115 120
 Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu
 125 130 135
 Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly
 140 145 150

Thr Thr Phe Pro	Leu Lys Asn Ala Glu	Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu	Asn Tyr Ile Ile Ser	Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg	Lys Arg Ser Asp Gly	Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys	Ala Leu Asp Arg Glu	Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr	Ala Leu Asp Gly Gly	Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val	Tyr Ile Glu Val Leu	Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu	Gln Pro Phe Tyr Arg	Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly	Phe Leu Val Val Lys	Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val	Asn Gly Glu Ile Ser	Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile	Gly Lys Thr Phe Lys	Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu	Lys Lys Gln Leu Asp	Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn	Ile Glu Ala Arg Asp	Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val	Leu Ile Gln Val Ile	Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr	Met Ser Ala Phe Thr	Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr	Val Val Ala Leu Phe	Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn	Gly Lys Ile Ser Cys	Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu	Lys Ser Ala Glu Asn	Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu	Asp Arg Glu Ser Arg	Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro	Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440	445	450	
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455	460	465	
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470	475	480	
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485	490	495	
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500	505	510	
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515	520	525	
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530	535	540	
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545	550	555	
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560	565	570	
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575	580	585	
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590	595	600	
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605	610	615	
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620	625	630	
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635	640	645	
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650	655	660	
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665	670	675	
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680	685	690	
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695	700	705	
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710	715	720	

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgtca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100
 cggtcgacga cgcgcccgcg tcatgcggct cctcggctgg tggcaagtat 150
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
 agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250
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 acagggcagc agaagaggcc aatgcggcgc tggggctgga cacccaaggc 350
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500
 cacttccttg acagagaaga ggagtattac acagagccag aagtggcggg 550
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 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
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 atcttcattt ttaatcagac aggtatagaa gccaagaaga atgtggtggt 1000
 aactcaagcc gaccaaatag gccctcttcc cagcactttg ataaaaagtg 1050
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 gcaggaacat gtggagtagt gatggctcga aagaagttgg aaagaggaaac 1200
 ttcaatcctt cgtttcagaa attagtcta cagtttcata cattttctcc 1250
 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttgttg 1300
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 caataagcaa atgcaaaaat attcaatag 1379

<211> 360
<212> PRT
<213> Homo sapiens

<400> 410

Met	Val	Pro	Ala	Ala	Gly	Arg	Arg	Pro	Pro	Arg	Val	Met	Arg	Leu	
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Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val	
				20					25					30	
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu	
				35					40					45	
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly	
				50					55					60	
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala	
				65					70					75	
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His	
				80					85					90	
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	
				95					100					105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	
				110					115					120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	
				125					130					135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	
				140					145					150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	
				155					160					165	
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg	
				170					175					180	
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	
				185					190					195	
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys	
				200					205					210	
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	
				215					220					225	
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	
				230					235					240	
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	
				245					250					255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly	

260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His	Thr Asp Arg Thr Leu Glu
275	280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln	Thr Gly Ile Glu Ala Lys
290	295	300
Lys Asn Val Val	Val Thr Gln Ala Asp	Gln Ile Gly Pro Leu Pro
305	310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp	Leu Leu Val Phe Ser Leu
320	325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr	Ala Thr Ile Arg Thr Glu
335	340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln	Glu Gln Glu His Val Glu
350	355	360

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgt cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgc tgtagcttag tcctgtttta caccctgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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His Cys Cys Leu Gly	Ser Ala Arg Gly	Leu Phe Leu Phe Gly	Gln
20		25	30
Pro Asp Phe Ser Tyr	Lys Arg Ser Asn Cys	Lys Pro Ile Pro	Val
35		40	45
Asn Leu Gln Leu Cys	His Gly Ile Glu Tyr	Gln Asn Met Arg	Leu
50		55	60
Pro Asn Leu Leu Gly	His Glu Thr Met Lys	Glu Val Leu Glu	Gln
65		70	75
Ala Gly Ala Trp Ile	Pro Leu Val Met Lys	Gln Cys His Pro	Asp
80		85	90
Thr Lys Lys Phe Leu	Cys Ser Leu Phe Ala	Pro Val Cys Leu	Asp
95		100	105
Asp Leu Asp Glu Thr	Ile Gln Pro Cys His	Ser Leu Cys Val	Gln
110		115	120
Val Lys Asp Arg Cys	Ala Pro Val Met Ser	Ala Phe Gly Phe	Pro
125		130	135
Trp Pro Asp Met Leu	Glu Cys Asp Arg Phe	Pro Gln Asp Asn	Asp
140		145	150
Leu Cys Ile Pro Leu	Ala Ser Ser Asp His	Leu Leu Pro Ala	Thr
155		160	165
Glu Glu Ala Pro Lys	Val Cys Glu Ala Cys	Lys Asn Lys Asn	Asp
170		175	180
Asp Asp Asn Asp Ile	Met Glu Thr Leu Cys	Lys Asn Asp Phe	Ala
185		190	195
Leu Lys Ile Lys Val	Lys Glu Ile Thr Tyr	Ile Asn Arg Asp	Thr
200		205	210
Lys Ile Ile Leu Glu	Thr Lys Ser Lys Thr	Ile Tyr Lys Leu	Asn
215		220	225
Gly Val Ser Glu Arg	Asp Leu Lys Lys Ser	Val Leu Trp Leu	Lys
230		235	240
Asp Ser Leu Gln Cys	Thr Cys Glu Glu Met	Asn Asp Ile Asn	Ala
245		250	255
Pro Tyr Leu Val Met	Gly Gln Lys Gln Gly	Gly Glu Leu Val	Ile
260		265	270
Thr Ser Val Lys Arg	Trp Gln Lys Gly Gln	Arg Glu Phe Lys	Arg
275		280	285
Ile Ser Arg Ser Ile	Arg Lys Leu Gln Cys		

<210> 416
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
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<210> 418
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 418
 ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<400> 419
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<210> 420
 <211> 560
 <212> PRT
 <213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg	1	5	10	15
Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp	20	25	30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	35	40	45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	50	55	60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	65	70	75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	80	85	90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	95	100	105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	110	115	120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	125	130	135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	140	145	150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	155	160	165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	170	175	180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met	185	190	195	
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	200	205	210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	215	220	225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	230	235	240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	245	250	255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu Leu	260	265	270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser Gly	275	280	285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala Leu	290	295	300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu Ala	305	310	315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro Phe	320	325	330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala Ala	335	340	345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro Val	350	355	360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu Gly	365	370	375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly Ile	380	385	390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser Glu	395	400	405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp Trp	410	415	420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe Ser	425	430	435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu Gln	440	445	450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly Gly	455	460	465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg Ala	470	475	480
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr Ala Arg	485	490	495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His Pro	500	505	510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala Thr	515	520	525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln Ala	530	535	540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
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Pro Trp Val Ile Thr
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<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag ccctcctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cgggtcaata aacctggacg cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtcccatatc ctgctcaact gggtcaggtc cctcttagac cagctcttgt 50

ccatcatttg ctgaagtgga ccaactagtt cccagtagg ggggtctccc 100

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tggccttgcc ttggggtcct gcttggttca taatcatcta actatgggac 200

aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250

tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggtt 300

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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met	Met	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Pro	Gly
1				5					10					15

Gly Tyr Leu Phe	Leu Leu Gly Asp Cys	Gln Glu Val Thr Thr	Leu
20	25		30
Thr Val Lys Tyr	Gln Val Ser Glu Glu	Val Pro Ser Gly Thr	Val
35	40		45
Ile Gly Lys Leu	Ser Gln Glu Leu Gly	Arg Glu Glu Arg Arg	Arg
50	55		60
Gln Ala Gly Ala	Ala Phe Gln Val Leu	Gln Leu Pro Gln Ala	Leu
65	70		75
Pro Ile Gln Val	Asp Ser Glu Glu Gly	Leu Leu Ser Thr Gly	Arg
80	85		90
Arg Leu Asp Arg	Glu Gln Leu Cys Arg	Gln Trp Asp Pro Cys	Leu
95	100		105
Val Ser Phe Asp	Val Leu Ala Thr Gly	Asp Leu Ala Leu Ile	His
110	115		120
Val Glu Ile Gln	Val Leu Asp Ile Asn	Asp His Gln Pro Arg	Phe
125	130		135
Pro Lys Gly Glu	Gln Glu Leu Glu Ile	Ser Glu Ser Ala Ser	Leu
140	145		150
Arg Thr Arg Ile	Pro Leu Asp Arg Ala	Leu Asp Pro Asp Thr	Gly
155	160		165
Pro Asn Thr Leu	His Thr Tyr Thr Leu	Ser Pro Ser Glu His	Phe
170	175		180
Ala Leu Asp Val	Ile Val Gly Pro Asp	Glu Thr Lys His Ala	Glu
185	190		195
Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe	Phe
200	205		210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
215	220		225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
230	235		240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
245	250		255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
260	265		270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser	Lys
275	280		285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
290	295		300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn	305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro Asn	320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp Val	335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln Pro	350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala Leu	365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val His	380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg Thr	395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp Arg	410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp Gln	425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln Ile	440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg Tyr	455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu Ile	470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys Val	485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala Ile	500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr	515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser	530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu	545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu	560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr	575	580	585

Gly His Leu Leu Val	Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
590		595	600
Ala Gly Thr Asp Thr	Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
605		610	615
Phe Leu Leu Thr Thr	Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
620		625	630
Asn Gly Glu Pro Leu	Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
635		640	645
Leu Phe Ile Leu Asn	Pro His Thr Gly	Gln Leu Phe Val Asn	Val
650		655	660
Thr Asn Ala Ser Ser	Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
665		670	675
Val Val Glu Asp Gln	Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
680		685	690
Leu Arg Val Met Phe	Val Thr Ser Val	Asp His Leu Arg Asp	Ser
695		700	705
Ala Arg Lys Pro Gly	Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
710		715	720
Cys Leu Ala Val Leu	Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
725		730	735
Phe Met Ser Ile Cys	Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
740		745	750
Asn Cys Arg Glu Ala	Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
755		760	765
Pro Gln Lys His Ile	Gln Lys Ala Asp	Ile His Leu Val Pro	Val
770		775	780
Leu Arg Gly Gln Ala	Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785		790	795
Lys Asp Val Asp Lys	Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800		805	810
Cys Leu Gln Ala Pro	Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815		820	825
Leu Arg Asn Gln Gly	Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830		835	840
Val Leu Gln Asp Thr	Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845		850	855
Arg Asn Ala Ser Arg	Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860		865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu
1175 1180

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaaagacag gccaggatcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser	35	40	45	
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe	50	55	60	
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp	65	70	75	
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val	80	85	90	
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu	95	100	105	
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe	110	115	120	
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	125	130	135	
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	140	145	150	
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	155	160	165	
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	170	175	180	
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln				

185					190					195				
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala
				200					205					210
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser
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Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly
				230					235					240
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu
				245					250					255
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala
				260					265					270
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr
				275					280					285
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys
				290					295					300
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys
				305					310					315
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu
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Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe
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Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu
				350					355					360
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Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr
				380					385					390
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu
				395					400					405
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn
				410					415					420
Phe	Tyr	His	Arg	Trp	Phe	Asp	Val	Ile	Phe	Leu	Val	Ser	Ala	Leu
				425					430					435
Ser	Ser	Ile	Leu	Phe	Leu	Tyr	Leu	Ala	His	Lys	Gln	Ala	Pro	Glu
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Lys	Gln	Met	Ala	Pro										
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<210> 431

<211> 407
<212> DNA
<213> Homo sapiens

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<222> 78, 81, 113, 157, 224, 297
<223> unknown base

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<210> 432
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<212> DNA
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<223> unknown base

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<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

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<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 434

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<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 435

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<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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				20					25					30

Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45

Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60

Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75

Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
				80					85					90

Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg
				95					100					105

Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu	Gly Val Ser Val Arg	Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala	380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly	680	685	690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro	695	700	705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met	710	715	720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro	725	730	735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val	740	745	750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr	755	760	765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr	770	775	780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu	785	790	795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro	800	805	810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser	815	820	825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val	830	835	840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln	845	850	855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro	860	865	870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val	875	880	885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser	890	895	900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg	905	910	915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu	920	925	930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu	935	940	945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn	950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

cgcgccgggc gcagggagct gaggtagcgg ctcgagacgg cggcgcgtgc 50

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ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcgagctg 200

ccgcggcggt ggctgcagcc ggggggcggt cggacggcgg taattttctg 250

gatgataaac aatgggtcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtgggtcta tcccagccct gtttgtggtt cagatgggtc 600

tacctactct ttccagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaagt gaaggacatt gcccatgtcc ttccagataag 700

cccaccagta caagcagaaa tgtaagaga gcatgcagtg acctggagtt 750

cagggaagtg gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800

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 aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050
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 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442
 <211> 436
 <212> PRT
 <213> Homo sapiens

<400> 442
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 20 25 30
 Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

35	40	45
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys		
50	55	60
Phe Arg Asp Glu Val Glu Asp Asp Tyr Phe Arg Thr Trp Ser Pro		
65	70	75
Gly Lys Pro Phe Asp Gln Ala Leu Asp Pro Ala Lys Asp Pro Cys		
80	85	90
Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp		
95	100	105
Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg		
110	115	120
Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile		
125	130	135
Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val		
140	145	150
Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu		
155	160	165
Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu		
170	175	180
Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg		
185	190	195
Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala		
200	205	210
Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser		
215	220	225
Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg		
230	235	240
Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp		
245	250	255
Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln		
260	265	270
Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr		
275	280	285
Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile		
290	295	300
Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro		
305	310	315
Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val		

	320		325		330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly	335		340		345
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp	350		355		360
Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn	365		370		375
Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe	380		385		390
Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu	395		400		405
Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu	410		415		420
Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr	425		430		435
Ile					

<210> 443
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 443
 cagcaatatt cagaagcggc aaggg 25

<210> 444
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 444
 catcatggtc atcaccacca tcatcatc 28

<210> 445
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100
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gctctgcctc cggtgctgct gcctggggcg gccggcttca caccttcct 200
cgatagcgac ttcaccttta cccttcccgc cggccagaag gagtgcttct 250
accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300
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aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400
ctgaagttagg tgattacatg ttctgctttg acaatacatt cagcaccatt 450
tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550
tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600
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ctatggttaa tttagtggtc atggtggtgg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800
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tttcctaact ttgaaaaatt ttgcaaattg cttaggtgat ttaaataaat 1100
gagtattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150
cccagaactt ttttgtaa at gcggcagtta caaattaact gtggaagttt 1200
tcagttttaa gttataaatc acctgagaat tacctaataa tggattgaat 1250

aaatccttag actacaaaag cccaactttt ctctatttac atatgcatct 1300
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taagtttatt tttaatagta tctgtcaagt taatatctgt caacagttaa 1650
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attaccagca gttatgaagg aatattgct aaaatgatct gggcctacca 1750
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agaatttaga aaaacttgag aaaacctaat ccaaaataaa attcacttaa 1850
gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900
tactcataac ataaatcaaa' ggagatgatt aatttccagt tagctggaag 1950
aaactttggc tgtaggtttt tattttctac aagaattctg gtttgaatta 2000
tttttgtaag caggtagatt ttataaaatg taagccctac tgtaagggtt 2050
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taaaatggcc tttctgaaca ctttatattt tgatgttgaa gtaaggatta 2150
gaaacataga ctcccaagtt ttaaacacct aaatgtgaat aacccatata 2200
tacaacaaag tttctgccat ctagcttttt gaagtctatg ggggtcttac 2250
tcaagtacta gtaatttaac ttcacatga atgaactata atttttaagt 2300
tatgcccatt tataacgttg tttatgacta cattgtgagt tagaaacaaa 2350
cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400
cttgatgagc aataatgata accagagagt gatttcattt aactcatag 2450
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cttagatttc cctactggca aggtttttta aaatgaggta aatgccgtat 2550
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 cataaccaa aaagcaaac ttgtaaacag agtaaaaatc tttaatattt 3050
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 gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcactctgaa 3500
 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50

agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100

gccctgcccc gtgtgtcctg gatgctgctt tcctgcctca ttctcctgtg 150

tcagggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200

gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttgttt 250

ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300

ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350

cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450

gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500

ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550

ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600

gttcaaggac tagggcaggt ggggaagtcag cagcctcagc ttggcgtgca 650

gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

ttctcccaa actgccctac ctgactacct tgtcatgac ctcttctttt 750

ttcttttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800

gagatctcag agaataataa taaaaatggt actttataaa aaaaaaaaaa 850

aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT
<213> Homo sapiens

<400> 452

Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu	
1				5					10					15	
Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln	
			20						25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
			35						40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
			50						55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
			65						70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
			80						85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
			95						100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
			110						115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
			125						130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
			140						145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
			155						160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
			170						175						

<210> 453
<211> 550
<212> DNA
<213> Homo sapiens

<400> 453

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ggcgctcctg gcgctgggtgc tggctgcctg cggagagctg gcgccggccc 150
tgcgctgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
ccgggagata gtgtaccctt tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400
tctgaacagc ctccactgcg gggccctcac gtcctccca ctcttgagcc 450
tccgactgta gagtccccgc ccacccccat ggccctatgc ggcccagccc 500
cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454
<211> 125
<212> PRT
<213> Homo sapiens

<400> 454
Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala
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Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
20 25 30
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
35 40 45
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
50 55 60
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
65 70 75
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
80 85 90
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
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Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
110 115 120
Leu Ser Leu Arg Leu
125

<210> 455
<211> 1518
<212> DNA
<213> Homo sapiens

<400> 455
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agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100
atcttctctt tctttctccc tcttgagtc ttctgagatg atggctctgg 150
gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggccgctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
 ttccaacgct atcaagaacc tgccccacc gctgggaggc gctgcggggc 300
 acccaggctc tgcagtcagc gccgcgcggg gaatcctgta cccgggaggc 350
 aataagtacc agaccattga caactaccag ccgtaccggt gcgcagagga 400
 cgaggagtgc ggcaactgat agtactgcgc tagtcccacc cgcggagggg 450
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 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
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 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000
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<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

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				20					25					30	
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu	
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Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val	
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Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln	
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Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
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Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
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Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
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Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
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Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
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Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
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509, 556
<223> unknown base

<400> 457
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<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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			20						25				30	
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu	80	85	90
Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu	95	100	105
Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr	110	115	120
Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu	125	130	135
Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe	140	145	150
Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala	155	160	165
Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg	170	175	180
Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met	185	190	195
Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly	200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu	215	220	225
Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu	230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala	245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys	260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu	275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn	290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg	305	310	315
Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn	320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu	335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe
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Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val
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Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr
695 700 705

Glu Arg Ala Lys Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg
710 715 720

Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr
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<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

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<210> 461

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

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<210> 462

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

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<210> 463

<211> 1818

<212> DNA

<213> Homo sapiens

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 <211> 300
 <212> PRT
 <213> Homo sapiens

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 Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu
 65 70 75
 Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr
 80 85 90
 Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn
 95 100 105
 Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn
 110 115 120
 Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu
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 140 145 150
 Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly

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185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly		
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Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys		
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln		
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln		
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<210> 465

<211> 1547

<212> DNA

<213> Homo sapiens

<400> 465

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cctggaacct gacgcagcg cactccagtt tttttatgac ctacgatttt 1450
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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
				20					25					30
Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
				35					40					45
Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
				50					55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser		65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln		80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp		95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln		110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser		125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro		140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala		155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg		170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro		185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala		200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys		215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys		230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe		245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe		260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro		275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe		290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu		305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His		320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu		335	340	345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp
410

<210> 467

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 467

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gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
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 ccataaaaaac gatttgcagc c 1071

<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468
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 20 25 30
 Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly
 35 40 45
 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
 50 55 60
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
 65 70 75
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
 80 85 90
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
 95 100 105
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
 110 115 120
 Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn
 125 130 135
 Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln
 140 145 150
 Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr
 155 160 165
 Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn
 170 175 180
 Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu
 185 190 195
 Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met
 200 205 210

Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly
 215 220 225

Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly
 230 235 240

Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys
 245 250 255

Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser
 260 265 270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
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 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
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 gtgcctgtgt ctgggctgtg tgaacccctt caccatgcag gaggaccgca 450
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 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
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 ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 470
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 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
 20 25 30

Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val	
				35					40					45	
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu	
				50					55					60	
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn	
				65					70					75	
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu	
				80					85					90	
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile	
				95					100					105	
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg	
				110					115					120	
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp	
				125					130					135	
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg	
				140					145					150	
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln	
				155					160					165	
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe	
				170					175					180	

<210> 471

<211> 2368

<212> DNA

<213> Homo sapiens

<400> 471

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ctccccgccg agaagcctcg ctcggcgccc aacatggcgg gtgggcgctg 150
cggccccgag ctaacggcgc tcttgccgc ctggatcgcg gctgtggcgg 200
cgacggcagg ccccaggag gccgcgtgc cgccggagca gagccgggtc 250
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cactctccca gcattttttc atgcaaagga tgggatattc cgccgttattc 500

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<210> 472
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 472
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 20 25 30
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
 35 40 45
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90
 Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val
 95 100 105
 Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg
 110 115 120
 Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile
 125 130 135
 Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys
 140 145 150
 Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser
 155 160 165

Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr	170	175	180
Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala	185	190	195
Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile	200	205	210
Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg	215	220	225
Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln	230	235	240
Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu	245	250	255
Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu	260	265	270
Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu	275	280	285
Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly	290	295	300
Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu	305	310	315
Glu Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr	320	325	330
Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala	335	340	345
Asp Lys Gly Leu			

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

gtccagccca tgaccgcctc caac 24

<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctcctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

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<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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caggggcaga aagaaaagag ctcccaaattg ctatatctat tcaggggctc 150
tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 2478

<210> 477
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 477
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 20 25 30
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
 35 40 45
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
 50 55 60
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser
 170 175 180
 Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
 185 190 195
 Glu Lys Lys Phe Ser Met
 200

<210> 478

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
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<210> 479
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 479
acaagtgtct tcccaacctg 20

<210> 480
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 480
atcctcccag agccatggta cctc 24

<210> 481
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
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<400> 481
ccaaggatag ctgttgtttc agagaaagga tcgtgtgctg catctcctcc 50
t 51

<210> 482
<211> 3819
<212> DNA
<213> Homo sapiens

<400> 482
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tcttggtcga tcgtaacctc cacctccggg gttcaagtga ttctcatgcc 150

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ccgtcggagg aaaatgactc cccagtcgct gctgcagacg acactgttcc 250
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 <211> 693
 <212> PRT
 <213> Homo sapiens

<400> 483

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Leu	Leu	Phe	Leu	Val	Gln	Gly	Ala	His	Gly	Arg	Gly	His	Arg	Glu
				20					25					30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
				35					40					45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
				50					55					60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
				65					70					75
Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe
				80					85					90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val	380	385	390
Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu	395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val	410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg	425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu	440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro	455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile	470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu	485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr	500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly	515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp	530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly	545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser	560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn	575	580	585
Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg	590	595	600
Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu	605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe	620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile	635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser	650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 68, 70, 84, 147
<223> unknown base

<400> 484
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cggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200
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tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450
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tttctgttca acatgg 516

<210> 485
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
ggcattggag cagtgcctgg tg 22

<210> 486
<211> 24
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

tggaggccta gatgcggctg gacg 24

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150

gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200

ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250

ccgccgtgag tgagctctca cccagtcag ccaaagagc ctcttcgggc 300

ttctcctgct gacatctgcc ctggccggcc agagacaggg gactcaggcg 350

gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400

cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450

gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500

ttggtatgga gattagtagc agtagaggaa aatgtatgga tacaacttac 550

gtttgatgaa agatttgggc ttgaagaccc agaagatgac atatgcaagt 600

atgattttgt agaagttgag gaaccagtg atggaactat attagggcgc 650

tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700

aattaggata agatttgtat ctgatgaata ttttccttct gaaccagggt 750

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe	20	25	30	
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	155	160	165	

Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala
				170					175					180
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser	Thr
				185					190					195
Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu
				200					205					210
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys
				215					220					225
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu
				230					235					240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe
				245					250					255
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe
				260					265					270
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala
				275					280					285
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys
				290					295					300
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr
				305					310					315
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu
				320					325					330
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly
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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

acttctcagt gtccataagg g 21

<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgct 40.

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

acaacaggca cagttccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 493

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<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 494

gcggctatcc tcctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	35	40	45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	50	55	60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	65	70	75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	80	85	90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	95	100	105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	110	115	120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	125	130	135	
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	140	145	150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	155	160	165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	170	175	180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	185	190	195	

Glu Lys Asp Ala Phe Leu Asn Leu Thr	Lys Leu Lys Val Leu Ser
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Leu Lys Asp Asn Asn Val Thr Ala Val	Pro Thr Val Leu Pro Ser
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Thr Leu Thr Glu Leu Tyr Leu Tyr Asn	Asn Met Ile Ala Lys Ile
230	235 240
Gln Glu Asp Asp Phe Asn Asn Leu Asn	Gln Leu Gln Ile Leu Asp
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Leu Ser Gly Asn Cys Pro Arg Cys Tyr	Asn Ala Pro Phe Pro Cys
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275	280 285
Phe Asp Ala Leu Thr Glu Leu Lys Val	Leu Arg Leu His Ser Asn
290	295 300
Ser Leu Gln His Val Pro Pro Arg Trp	Phe Lys Asn Ile Asn Lys
305	310 315
Leu Gln Glu Leu Asp Leu Ser Gln Asn	Phe Leu Ala Lys Glu Ile
320	325 330
Gly Asp Ala Lys Phe Leu His Phe Leu	Pro Ser Leu Ile Gln Leu
335	340 345
Asp Leu Ser Phe Asn Phe Glu Leu Gln	Val Tyr Arg Ala Ser Met
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Asn Leu Ser Gln Ala Phe Ser Ser Leu	Lys Ser Leu Lys Ile Leu
365	370 375
Arg Ile Arg Gly Tyr Val Phe Lys Glu	Leu Lys Ser Phe Asn Leu
380	385 390
Ser Pro Leu His Asn Leu Gln Asn Leu	Glu Val Leu Asp Leu Gly
395	400 405
Thr Asn Phe Ile Lys Ile Ala Asn Leu	Ser Met Phe Lys Gln Phe
410	415 420
Lys Arg Leu Lys Val Ile Asp Leu Ser	Val Asn Lys Ile Ser Pro
425	430 435
Ser Gly Asp Ser Ser Glu Val Gly Phe	Cys Ser Asn Ala Arg Thr
440	445 450
Ser Val Glu Ser Tyr Glu Pro Gln Val	Leu Glu Gln Leu His Tyr
455	460 465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser	Cys Arg Phe Lys Asn Lys
470	475 480

Glu Ala Ser Phe	Met Ser Val Asn Glu	Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp	Leu Ser Lys Asn Ser	Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln	His Leu Ser Phe Leu	Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile	Ser Gln Thr Leu Asn	Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu	Arg Tyr Leu Asp Phe	Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser	Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser	Ser Asn Ser His Tyr	Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu	Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn	Asp Asn Asp Ile Ser	Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu	Ser Leu Arg Thr Leu	Glu Phe Arg Gly Asn His	620	625	630
Leu Asp Val Leu	Trp Arg Glu Gly Asp	Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu	Leu Lys Leu Glu Glu	Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe	Leu Pro Ser Gly Val	Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn	Leu Ser Leu Ala Lys	Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys	Leu Gln Cys Leu Lys	Asn Leu Glu Thr Leu Asp	695	700	705
Leu Ser His Asn	Gln Leu Thr Thr Val	Pro Glu Arg Leu Ser Asn	710	715	720
Cys Ser Arg Ser	Leu Lys Asn Leu Ile	Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr	Lys Tyr Phe Leu Gln	Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu	Ser Ser Asn Lys Ile	Gln Met Ile Gln Lys Thr	755	760	765

Ser	Phe	Pro	Glu	Asn	Val	Leu	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu	770	775	780
His	His	Asn	Arg	Phe	Leu	Cys	Thr	Cys	Asp	Ala	Val	Trp	Phe	Val	785	790	795
Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	800	805	810
Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	815	820	825
Ile	Ser	Leu	Asp	Leu	Tyr	Thr	Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	830	835	840
Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val	845	850	855
Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	Tyr	Ile	860	865	870
Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	Ile	875	880	885
Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys	890	895	900
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	905	910	915
Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu	920	925	930
Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	935	940	945
Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	950	955	960
Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	965	970	975
Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	980	985	990
Leu	Glu	Lys	Pro	Phe	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	995	1000	1005
Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	1010	1015	1020
Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr	1025	1030	1035
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<210> 497
<211> 4199
<212> DNA
<213> Homo sapiens

<400> 497
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
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Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
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Asp Phe Lys Gly Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser Gly
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260	265 270
Asp Gly Gly Ala Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln Asn
275	280 285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu Arg
290	295 300
Lys Ile Asn Ala Ala Trp Phe Lys Asn	Met Pro His Leu Lys Val
305	310 315
Leu Asp Leu Glu Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser Gly
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Ala Phe Leu Thr Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu Ser
335	340 345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile Ser
350	355 360
Arg Asn Phe Ser Lys Leu Leu Ser Leu	Arg Ala Leu His Leu Arg
365	370 375
Gly Tyr Val Phe Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro Leu
380	385 390
Met Gln Leu Pro Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn Phe
395	400 405
Ile Lys Gln Ile Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn Leu
410	415 420
Glu Ile Ile Tyr Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val Lys
425	430 435
Asp Thr Arg Gln Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg His
440	445 450
Ile Arg Lys Arg Arg Ser Thr Asp Phe	Glu Phe Asp Pro His Ser
455	460 465
Asn Phe Tyr His Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys Ala
470	475 480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe Phe
485	490 495
Ile Gly Pro Asn Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys Leu
500	505 510
Asn Leu Ser Ala Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr Glu
515	520 525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu Asp	635	640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	650	655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	665	670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	680	685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	695	700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	710	715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	725	730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	740	745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	755	760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	770	775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	785	790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	800	805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
Asp Ser Ile Lys Gln Tyr	1040		

<210> 499

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 499
taaagaccca gctgtgaccg 20

<210> 500
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 500
atccatgagc ctctgatggg 20

<210> 501
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 501
atttatgtct cgaggaaagg gactggttac cagggcagcc agttc 45

<210> 502
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 502
gccgagacaa aaacgttctc c 21

<210> 503
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 503
catccatggt ctcattccatt agcc 24

<210> 504
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 504
tcgacaacct catgcagagc atcaacccaaa gcaagaaaac agtatt 46

<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 505

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ctagagatcc ctgcacctcg acccacgcgt ccgccaagct ggccctgcac 100
ggctgcaagg gaggctcctg tggacaggcc aggcaggtgg gcctcaggag 150
gtgcctccag gcggccagtg ggcctgaggc ccagcaagg gctaggggtcc 200
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250
cagcagcatc agcagcccc aggaccggg aggcacaggt ggccccacc 300
acccggagga gcagctcctg ccctgtccg ggggatgact gattctctc 350
cgccaggcca ccagaggag aaggccacc cgctggagg cacaggccat 400
gaggggctct caggagggtc tgctgatgtg gcttctggtg ttggcagtgg 450
gcggcacaga gcacgcctac cgccccggc gtaggggtg tgctgtccg 500
gtcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550
cttcctcacc acctgcgacg ggcaccggg ctgcagcacc taccgaacca 600
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cgctacgcgt gctgccccgg ctggaagagg accagcgggc ttcctggggc 700
ctgtggagca gcaatatgcc agccgccatg ccggaacgga gggagctgtg 750
tccagcctgg ccgtgccgc tgccctgcag gatggcgggg tgacacttgc 800
cagtcagatg tggatgaatg cagtgctagg aggggcggct gtccccagcg 850
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gcctgtctgc agacggtaca ctctgtgtgc ccaagggagg gccccccagg 950
gtggccccca acccgacagg agtggacagt gcaatgaagg aagaagtgc 1000
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 agctccctgc tggagcctgg gacccatggc acaggccagg cagcccggag 1550
 gctgggtggg gcctcagtgg gggctgctgc ctgaccccca gcacaataaa 1600
 aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
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 gcccaacttg ttattgcag cttataatgg ttacaaat 1738

<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu	1	5	10	15
Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	20	25	30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu				

155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys Gly	
170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro	Thr Gly Val Asp Ser Ala	
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln	Ser Arg Val Asp Leu Leu	
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala	Pro Leu His Ser Leu Ala	
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro	Asp Pro Gly Ser Leu Leu	
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser Glu	
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys Lys	
260	265	270

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507
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 tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttcgcgcta 200
 cgccctgcgg tgtcccagg gctgaggtct cctcatcttc tccctagcag 250
 tggatgagca acccaacggg ggcccgggga ggggaactgg ccccagaggga 300
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 gcagccccca ggaccgggga ggcacaggtg gccccacca cccggaggag 400
 cagctcctgc cctgtccgg gggatgactg attctcctcc gccaggccac 450
 ccagaggaga aggccacccc gcctggaggc acaggccatg aggggctctc 500
 aggaggtgct gctgatgtgg cttctggtgt tggcagtggg cggcacagag 550
 cagcctacc ggcccggccg tagggtgtgt gctgtccggg ctacgggga 600
 ccctgtctcc gagtcgttcg tgcagcgtgt gtaccagccc ttcctcacca 650

cctgcgacgg gcaccggggc tgcagcacct accgaaccat ctataggacc 700
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 ctgccccggc tggaagagga ccagcgggct tccctggggc tgtggagcag 800
 caatatgcca gccgccatgc cggaacggag ggagctgtgt ccagcctggc 850
 cgctgccgct gccctgcagg atggcggggt gacacttgcc agtcagatgt 900
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 ccgccggcag ttactggtgc cagtgttggg aggggcacag cctgtctgca 1000
 gacggtacac tctgtgtgcc caagggaggg cccccaggg tggccccaa 1050
 cccgacagga gtggacagtg caatgaagga agaagtgcag aggctgcagt 1100
 ccagggtgga cctgctggag gagaagctgc agctggtgct ggccccactg 1150
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 tcccaaggcc aggtggaccc tcagctgagg gaaggtacga gctccctgct 1600
 ggagcctggg acccatggca caggccaggc agcccggagg ctgggtgggg 1650
 cctcagtggg ggctgctgcc tgacccccag cacaataaaa atgaaacgtg 1700

<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
1				5					10				15	

Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25				30	

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35				40					45	

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	
				260					265					270	

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

cccacgcgtc cgaagctggc cctgcacggc tgcaaggag gctcctgtgg 50

acaggccagg caggtgggcc tcaggaggtg cctccaggcg gccagtgggc 100
ctgaggcccc agcaagggtt aggggtccatc tccagtccca ggacacagca 150
gcggccacca tggccacgcc tgggtccag cagcatcagc agccccagg 200
accggggagg cacaggtggc cccaccacc cggaggagca gtcctgccc 250
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gccacccgc ctggaggcac aggccatgag gggctctcag gaggtgctgc 350
tgatgtggct tctggtgttg gcagtgggcg gcacagagca cgcctaccgg 400
cccggccgta ggggtgtgtg tgtccgggtt cacggggacc ctgtctccga 450
gtcgttcgtg cagcgtgtgt accagccctt cctcaccacc tgcgacgggc 500
accgggcctg cagcacctac cgaaccatct ataggaccgc ctaccgccc 550
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cgccatgccg gaacggaggg agctgtgtcc agcctggccg ctgccgctgc 700
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gtgggcccctc agctgaggga aggtacgagc tccctgctg agcctgggac 1450
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ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
1				5					10					15

Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165

Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180

Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195

Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225

Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

tggagcagca atatgccagc c 21

<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 514

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ggagacagcc tcccggcccg gggaggacaa gtcgctgcca cctttggctg 100

ccgacgtgat tccctgggac ggtccgtttc ctgccgtcag ctgccggccg 150
agttgggtct ccgtgtttca ggccggctcc ccttctctgg tctcccttct 200
cccgtgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350
cattttggag caggaattcc aatcatgtct gtgatgggtg tgagaaagaa 400
ggtgacacgg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450
atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500
ttcctcatcc tggggacatg tacactcttc ttgcctttg agtgccgcta 550
cctggctgtt cagctgtctc ctgccatccc tgtatttgct gccatgctct 600
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tcaagaatth ccagataaac aaccagattg tgaaactgaa atactgttac 800
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

	305		310		315
Glu Thr Ser Ser	Ser Leu Leu Pro Gln	Ser Pro Ala Pro Thr	Glu		
	320		325		330
His Leu Asn Ser	Asn Glu Met Pro Glu	Asp Ser Ser Thr Pro	Glu		
	335		340		345
Glu Met Pro Pro	Pro Glu Pro Pro Glu	Pro Pro Gln Glu Ala	Ala		
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Glu Ala Glu Lys

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
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 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 517
 caacgtgatt tcaaagctgg gctc 24

<210> 518
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg ccggtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

gtgcactatt gacaaccggg taccgggtt ggcttggtta aaccgcagca 350

ccatcctcta tgctgggaat gacaagtggt gcctggatcc tcgcgtggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450
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 gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600
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<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro	
				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
				95					100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
				110					115					120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
				125					130					135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
				140					145					150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
				170					175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	
				230					235					240	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
				245					250					255	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
				260					265					270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
				275					280					285	

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
 290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
 305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
 320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
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<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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<210> 525

<211> 2602

<212> DNA

<213> Homo sapiens

<400> 525

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 tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150
 aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctggtctt 200
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ccctaggggt ccagtaccac agagacccat cccacagcac ctgccttaca 300
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<210> 526
 <211> 736
 <212> PRT
 <213> Homo sapiens

<400> 526
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 20 25 30
 Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu
 35 40 45
 Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro
 50 55 60

Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly	
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Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp	
				80					85					90	
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	
				95					100					105	
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp	
				110					115					120	
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	
				125					130					135	
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu	
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Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro	
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Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly	
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Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala	
				185					190					195	
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala	
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Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser	
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				260					265					270	
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val	
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Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met	
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Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu	
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Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser	
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Glu	Pro	Val	Val	Val	Tyr	Gly	Met	Asp	Tyr	Leu	Gln	Gln	Val	Ser	
				335					340					345	

Glu Leu Ile Asn Arg Thr Glu Pro Ser	Ile Leu Asn Asn Tyr Leu
350	355 360
Ile Trp Asn Leu Val Gln Lys Thr Thr	Ser Ser Leu Asp Arg Arg
365	370 375
Phe Glu Ser Ala Gln Glu Lys Leu Leu	Glu Thr Leu Tyr Gly Thr
380	385 390
Lys Lys Ser Cys Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn Thr
395	400 405
Asp Asp Ala Leu Gly Phe Ala Leu Gly	Ser Leu Phe Val Lys Ala
410	415 420
Thr Phe Asp Arg Gln Ser Lys Glu Ile	Ala Glu Gly Met Ile Ser
425	430 435
Glu Ile Arg Thr Ala Phe Glu Glu Ala	Leu Gly Gln Leu Val Trp
440	445 450
Met Asp Glu Lys Thr Arg Gln Ala Ala	Lys Glu Lys Ala Asp Ala
455	460 465
Ile Tyr Asp Met Ile Gly Phe Pro Asp	Phe Ile Leu Glu Pro Lys
470	475 480
Glu Leu Asp Asp Val Tyr Asp Gly Tyr	Glu Ile Ser Glu Asp Ser
485	490 495
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Met Ala Asp Gln Leu Arg Lys Pro Pro	Ser Arg Asp Gln Trp Ser
515	520 525
Met Thr Pro Gln Thr Val Asn Ala Tyr	Tyr Leu Pro Thr Lys Asn
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Glu Ile Val Phe Pro Ala Gly Ile Leu	Gln Ala Pro Phe Tyr Ala
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Arg Asn His Pro Lys Ala Leu Asn Phe	Gly Gly Ile Gly Val Val
560	565 570
Met Gly His Glu Leu Thr His Ala Phe	Asp Asp Gln Gly Arg Glu
575	580 585
Tyr Asp Lys Glu Gly Asn Leu Arg Pro	Trp Trp Gln Asn Glu Ser
590	595 600
Leu Ala Ala Phe Arg Asn His Thr Ala	Cys Met Glu Glu Gln Tyr
605	610 615
Asn Gln Tyr Gln Val Asn Gly Glu Arg	Leu Asn Gly Arg Gln Thr
620	625 630

Leu Gly Glu Asn Ile Thr Asp Asn Gly Gly Leu Lys Ala Ala Tyr	635	640	645
Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln	650	655	660
Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly	665	670	675
Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His	680	685	690
Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val	695	700	705
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gagagagggga aggcagctat gtc 23

<210> 566

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<223> Synthetic oligonucleotide probe

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<210> 567

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<223> Synthetic oligonucleotide probe

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<211> 22

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

<400> 581

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<210> 582

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cccccaagcc cttagactct aagcc 25

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gacccggcac cttgctaac 19

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<400> 596

ggctctgagt ctctgcttga 20

<210> 597

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 597

tccaacaacc attttcctct ggtcc 25

<210> 598

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 598
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<210> 599
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caagcgtcca ggtttattga 20

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gactacaagg cgctcagcta 20

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ccggctgggt ctcaactcctc c 21

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cgactccctg agcgagcaga tttcc 25

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<210> 611
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<213> Homo Sapien

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accacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200
ctgtggcgcg ccgcctgggt cccgggaaga ctgccagca ccagggggtg 250
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<210> 612
 <211> 352
 <212> PRT
 <213> Homo Sapien

<400> 612
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 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn
 35 40 45
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
 50 55 60
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn	Asp Met Thr Val Asn Glu	
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu Ala	Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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aaataagaaa atttcaagg aggacgagct cttgagttag acccaacaag 150
ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200
cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250
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atctgcaggc gcggtccgg gtcctggaga tgtatttcct caatgacact 350
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tggaagacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450
aactcacctg ggtccgcgtc agccatgagc acttgctgca gcgggtagac 500
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cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600
gcccgcggg accacctgct gagaaggag ccaagggggc tatgggacga 650
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agaggcgggc ctccaaggac ccaggggtgc tccagggaag caaggagcca 750
ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800
ctcattggcc caaaagggga aactggaact aaggagaga aaggagacct 850
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aggatcttct ggggagcaag gagtaaagg agaaaaagg gaaagaggtg 1350
aaaactcagt gtccgtcagg attgtcgga gtagtaacc aggccgggct 1400
gaagtttact acagtggtag ctgggggaca atttgcgat acgagtggca 1450

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 ctggggccat catgactgca gccacgagga ggacgcaggc gtggagtgca 1650
 gcgtctgacc cggaaccct ttcacttctc tgctcccagag gtgtcctcgg 1700
 gctcatatgt gggaaggcag aggatctctg aggagttccc tggggacaac 1750
 tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

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Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln				

185	190	195
Gly Pro Pro Gly Val Lys Gly Glu Ala	Gly Leu Gln Gly Pro Gln	
200	205	210
Gly Ala Pro Gly Lys Gln Gly Ala Thr	Gly Thr Pro Gly Pro Gln	
215	220	225
Gly Glu Lys Gly Ser Lys Gly Asp Gly	Gly Leu Ile Gly Pro Lys	
230	235	240
Gly Glu Thr Gly Thr Lys Gly Glu Lys	Gly Asp Leu Gly Leu Pro	
245	250	255
Gly Ser Lys Gly Asp Arg Gly Met Lys	Gly Asp Ala Gly Val Met	
260	265	270
Gly Pro Pro Gly Ala Gln Gly Ser Lys	Gly Asp Phe Gly Arg Pro	
275	280	285
Gly Pro Pro Gly Leu Ala Gly Phe Pro	Gly Ala Lys Gly Asp Gln	
290	295	300
Gly Gln Pro Gly Leu Gln Gly Val Pro	Gly Pro Pro Gly Ala Val	
305	310	315
Gly His Pro Gly Ala Lys Gly Glu Pro	Gly Ser Ala Gly Ser Pro	
320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	

470

475

480

Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu
 485 490 495

Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His
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Glu Glu Asp Ala Gly Val Glu Cys Ser Val
 515 520

<210> 615

<211> 647

<212> DNA

<213> Homo Sapien

<400> 615

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 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350
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 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
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<210> 616

<211> 98

<212> PRT

<213> Homo Sapien

<400> 616

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 20 25 30

Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45

Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
50 55 60

Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
65 70 75

Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
80 85 90

Phe Val Ile Pro Cys Asn Asn Gln
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<210> 617

<211> 2558

<212> DNA

<213> Homo Sapien

<400> 617

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cgaaaccgac tcggctgtgg ccaccgcgc cgcggcggc tggctgtgcg 250
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cagaagaatt tggctcttctt ggttctactg agtgggcaga ggagaattca 1500
agactccttc aagagcgtgg cgtggcttat attaatgctg actcatctat 1550
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<210> 618
 <211> 750
 <212> PRT
 <213> Homo Sapien

<400> 618

Met	Trp	Asn	Leu	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Thr	Ala	1	5	10	15
Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly	20	25	30	
Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser	35	40	45	
Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala	50	55	60	
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His	65	70	75	
Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	80	85	90	
Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	95	100	105	
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	110	115	120	
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	125	130	135	
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	140	145	150	
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	155	160	165	
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	170	175	180	
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	185	190	195	
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	200	205	210	

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val
215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys
230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg
245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro
260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu
275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr
290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro
305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly
320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His
335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly
350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly
365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser
380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu
395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser
410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala
425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile
440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp
455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu
470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu
485	490	495

Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro
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 Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe
 515 520 525
 Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn
 530 535 540
 Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val
 545 550 555
 Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe
 560 565 570
 Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Gly Met Val Phe
 575 580 585
 Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr
 590 595 600
 Ala Val Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser
 605 610 615
 Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp
 620 625 630
 Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys
 635 640 645
 Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val
 650 655 660
 Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala Phe
 665 670 675
 Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val
 680 685 690
 Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe
 695 700 705
 Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
 710 715 720
 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala
 725 730 735
 Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
 740 745 750

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 620
<211> 25
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<220>
<223> Synthetic oligonucleotide probe

<400> 620
gaacatcagc gctcccggta attcc 25

<210> 621
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622
<211> 25
<212> DNA
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<220>
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<400> 622
ccaaactcac ccagtgagtg tgagc 25

<210> 623
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<212> DNA
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<220>
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<400> 623
tgggaaatca ggaatggtgt tctcc 25

<210> 624
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide probe

<400> 624

cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50